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L1
                E GEDULIN B/AU
             22 S E3, E6, E7
L2
                 E YOUNG A/AU
            111 S E3, E4
L3
            103 S E141, E142
L4
               3 S E159
L5
                 E AMYLIN/PA, CS
             143 S E3-E29
L6
             16 S L1-L6 AND EXENDIN?
L7
      FILE 'REGISTRY' ENTERED AT 10:00:10 ON 29 DEC 2003
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 L10
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 L11
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 L12
                9 S L12 AND P/DT
 L13
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 L14
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 L15
              124 S L15 AND 39-40/SQL
 L16
               16 S L15 NOT L16
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                0 S L19 AND 38-40/SQL
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  L20
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  L21
               21 S E3
  L22
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                10 S L25, L26 AND (PY<=1999 OR PRY<=1999 OR AY<=1999)
                 7 S L25 AND L1-L6
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                11 S L27, L29
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        FILE 'USPATFULL, USPAT2' ENTERED AT 10:16:37 ON 29 DEC 2003
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FILE 'REGISTRY' ENTERED AT 10:17:16 ON 29 DEC 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

28 DEC 2003 HIGHEST RN 631841-90-2 DICTIONARY FILE UPDATES: 28 DEC 2003 HIGHEST RN 631841-90-2

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

A Company of the Comp

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELF CROSSOVER for details.

Experimental and calculated property data are now available. For more information enter HELP PROP at an arrow prompt in the file or refer to the file summary sheet on the web at: http://www.cas.org/ONLINE/DBSS/registryss.html

140 SEA FILE=REGISTRY ABB=ON PLU=ON [HRT][SGAT][DE]GT[FYA][TS][TS][DE][LIVMG'UND']SKQ[LIVMG'UND']EEEAVRL[FYA][IVLMG'UND'][DE][WF => d sta que 116 L15

124 SEA FILE=REGISTRY ABB=ON PLU=ON L15 AND 39-40/SQL L16

42 SEA FILE=REGISTRY ABB=ON PLU=ON [SGAT][DE]GT[FYA][TS][TS][DE] [LIVMG'UND']SKQ[LIVMG'UND']EEEAVRL[FYA][IVLMG'UND'][DE][WFYA]LK => d sta que 118 .{0,1}[KN]GG.SSGA..../SQSP

FILE 'HCAPLUS' ENTERED AT 10:17:39 ON 29 DEC 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

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FILE COVERS 1907 - 29 Dec 2003 VOL 140 ISS 1 FILE LAST UPDATED: 28 Dec 2003 (20031228/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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Was Burn Care

L30 ANSWER 1 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN

2003:355827 HCAPLUS AN

Novel exendin agonist formulations and methods of administration there 138:374157 Entered STN: 09 May 2003 DN EDTI

\$ 11 July 3

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M. Jan

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U.S. Pat. Appl. Publ., 104 pp., Cont.-in-part of U.S. Ser. No. 889,330.
     Young, Andrew A.; Kolterman, Orville G.
IN
PA
      CODEN: USXXCO
SO
       Patent
DT
       English
       ICM A61K038-17
 LA
 IC
                                                                           DATE
       514012000
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                                                      _____
                                                                           20020528 <--
 CC
                                    DATE
                                                     US 2002-157224
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                    DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
                    CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
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1999-116380P P 19990114
        PRAI US 1999-116380P
                                          20000110
                                    Р
              US 2000-175365P
               Novel exendin and exendin agonist compound formulations and dosages and
                                          20000114
               methods of administration thereof are provided. These compns. and methods
              WO 2000-US902
               methods of admitted ton thereof are provided. These compns. and methods are useful in treating diabetes and conditions that would be benefited by
              US 2001-889330
               lowering plasma glucose or delaying and/or slowing gastric emptying or
         AB
                exendin agonist formulation antidiabetic
                inhibiting food intake.
                Antidiabetic agents
                 Cardiovascular system, disease
          ST
                     (exendin agonist formulations and methods of administration thereof)
          IT
                 Diabetes mellitus
                      (intratracheal; exendin agonist formulations and methods of
                 Human
                  Protein sequences
                  Drug delivery systems
                       (oral; exendin agonist formulations and methods of administration
                      administration thereof)
            TI
                   Drug delivery systems
                       (parenterals; exendin agonist formulations and methods of
             IT
                       thereof)
                    Drug delivery systems
                        (sublingual; exendin agonist formulations and methods of administration
              IT
                       administration thereof)
                    Drug delivery systems
              IT
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thereof) IT Drug delivery systems (sustained-release; exendin agonist formulations and methods of administration thereof) IT Drug delivery systems (transdermal; exendin agonist formulations and methods of administration thereof) ΙT Drug delivery systems (transmucosal; exendin agonist formulations and methods of administration thereof) 522007-58-5 522007-56-3 522007-60-9 IT 522007-52-9 RL: PRP (Properties) (Unclaimed; novel exendin agonist formulations and methods of administration thereof) ΙT 213190-65-9, Exendin RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (agonists; exendin agonist formulations and methods of administration thereof) 89750-14-1, Glucagon-like peptide I 141732-76-5, Exendin 4 TT RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (exendin agonist formulations and methods of administration thereof) ΙT 521986-08-3 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (unclaimed protein sequence; exendin agonist formulations and methods of administration thereof) 522007-07-4 522007-08-5 IT 522007-04-1 522007-05-2 522007-06-3 522007-09-6 522007-10-9 522007-11-0 522007-14-3 522007-12-1 522007-13-2 522007-15-4 522007-16-5 522007-17-6 522007-19-8 522007-20-1 522007-21-2 522007-18-7 522007-22-3 522007-23-4 **522007-24-5 522007-25-6** 522007-27-8 **522007-28-9 522007-29-0** 522007-26-7 522007-30-3 522007-31-4 522007-32-5 522007-34-7 522007-35-8 522007-36-9 522007-37-0 522007-33-6 522007-41-6 522007-42-7 522007-40-5 522007-38-1 522007-39-2 522007-47-2 522007-43-8 522007-44-9 522007-45-0 522007-46-1 522007-49-4 522007-50-7 522007-51-8 522007-53-0 522007-48-3 522007-59-6 522007-55-2 522007-57-4 522007-61-0 522007-54-1 522007-64-3 522007-65-4 522007-66-5 522007-62-1 522007-63**-**2 522007-68-7 522007-69-8 522007-70-1 522007-71-2 522007-67-6 522007-74-5 522007-75-6 522007-72-3 522007-73-4 522007-76-7 522007-80-3 522007-81-4 522007-79-0 522007-77-8 522007-78-9 RL: PRP (Properties) (unclaimed protein sequence; novel exendin agonist formulations and methods of administration thereof) 165338-05-6, 1-31-Exendin 4 (Heloderma suspectum) 210712-28-0, IT 238091-56-0 238091-57-1 1-30-Exendin 4 (Heloderma suspectum) 238091-60-6 238091-61-7 238091-62-8 238091-59-3 238091-58-2 238091-65-1 238091-66-2 238091-67-3 238091-64-0 238091-63-9 238091-69-5 238091-70-8 238091-71-9 238091-72-0 238091-68-4 238091-73-1 238091-74-2 238091-75-3 238091-76-4 238091-77-5 238091-79-7 238091-80-0 238091-81-1 238091-82-2 238091-78-6 238091-84-4 238091-86-6 238091-87-7 238091-88-8 238091-83-3 238091-92-4 238091-93-5 238091-94-6 351208-37-2 351208-40-7 351208-41-8 351208-42-9 351208-43-0 351208-44-1 351208-45-2 351208-46-3 351208-47-4 351208-48-5 351208-49-6 351208-50-9 351208-53-2 351208-54-3 351208-55-4 351208-56-5 351208-57-6 351208-59-8 351208-60-1 351208-61-2 351208-62-3 351208-58**-**7 351208-67-8 351208-68-9 351208-69-0 351208-65-6 351208-66-7

351208-74-7

351208-78-1

351208-79-2

351208-70**-**3

351208-72-5

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        (unclaimed sequence; novel exendin agonist formulations and methods of
        administration thereof)
    ANSWER 2 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
L30
     2001:525943 HCAPLUS
AN
DN
     135:132445
     Entered STN: 20 Jul 2001
ED
     Use of exendins and agonists thereof for modulation of triglyceride levels
TΙ
     and treatment of dyslipidemia
     Kolterman, Orville Gene; Young, Andrew A.
IN
     Amylin Pharmaceuticals, Inc., USA
PΑ
     PCT Int. Appl., 161 pp.
SO
     CODEN: PIXXD2
DT
     Patent
     English
LA
IC
     ICM A61K038-22
          A61P003-06; A61K038-22; A61K031-20; A61K038-22; A61K031-22;
          A61K038-22; A61K031-365; A61K038-22; A61K031-40
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FAN.CNT 4
                       KIND
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                                            WO 2001-US719
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PRAI US 2000-175365P
                        Р
                             20000110
                             20010109
     WO 2001-US719
                        W
     Methods for modulating the levels of plasma triglyceride and other lipids
AΒ
     in a subject comprise administration of an effective amount of an exendin or
     exendin agonist, alone or in conjunction with other compds. or compns.
     that lower blood triglyceride and/or other lipid levels.
     hypolipidemic triglyceride dyslipidemia treatment exendin
ST
     Antidiabetic agents
IT
     Heart, disease
     Hypolipemic agents
         (exendins and agonists for modulation of triglyceride levels and
        treatment of dyslipidemia)
     Glycerides, biological studies
ΙT
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
         (exendins and agonists for modulation of triglyceride levels and
        treatment of dyslipidemia)
ΙT
     Drug delivery systems
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(injections, s.c.; exendins and agonists for modulation of triglyceride
        levels and treatment of dyslipidemia)
IT
     Drug delivery systems
        (injections; exendins and agonists for modulation of triglyceride
        levels and treatment of dyslipidemia)
IT
     Diabetes mellitus
        (non-insulin-dependent; exendins and agonists for modulation of
        triglyceride levels and treatment of dyslipidemia)
TT
     210712-29-1
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     study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL
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        (exendins and agonists for modulation of triglyceride levels and
        treatment of dyslipidemia)
IT
     130391-54-7, Exendin 3
                               141732-76-5, Exendin 4
                                                        213190-65-9, Exendin
     213190-65-9D, Exendin, analogs and derivs.
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     (Uses)
        (exendins and agonists for modulation of triglyceride levels and
        treatment of dyslipidemia)
IT
     50-99-7, D-Glucose, biological studies
                                               9007-92-5, Glucagon, biological
     studies
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (exendins and agonists for modulation of triglyceride levels and
        treatment of dyslipidemia)
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        (unclaimed protein sequence; use of exendins and agonists thereof for
        modulation of triglyceride levels and treatment of dyslipidemia)
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     1-30-Exendin 4 (Heloderma suspectum)
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        (unclaimed sequence; use of exendins and agonists thereof for
       modulation of triglyceride levels and treatment of dyslipidemia)
             THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
RE
(1) Amylin Pharmaceuticals Inc; WO 9830231 A 1998 HCAPLUS
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(3) Andersson, K; WO 9962872 A 1999 HCAPLUS
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    ANSWER 3 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
L30
    2000:861704 HCAPLUS
AN
    134:37033
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ED
    Use of exendins and agonists thereof for the treatment of gestational
ΤI
     diabetes mellitus
    Hiles, Richard; Prickett, Kathryn S.
ΙN
    Amylin Pharmaceuticals, Inc., USA
PA
    PCT Int. Appl., 133 pp.
SO
    CODEN: PIXXD2
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    ICM C07K014-00
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     1-10 (Pharmacology)
     Section cross-reference(s): 34
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    Methods for treating gestational diabetes which comprise administration of
AΒ
     an effective amount of an exendin or an exendin agonist, alone or in
     conjunction with other compds. or compns. that lower blood glucose levels.
     exendin agonist gestational diabetes mellitus treatment
ST
ΤT
     Pregnancy
        (gestational diabetes mellitus; use of exendins and agonists thereof
        for treatment of gestational diabetes mellitus in relation to
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combination with insulin or amylin agonist)

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IT
    Diabetes mellitus
        (gestational; use of exendins and agonists thereof for treatment of
        gestational diabetes mellitus in relation to combination with insulin
        or amylin agonist)
IT
    Antidiabetic agents
     Drug interactions
        (use of exendins and agonists thereof for treatment of gestational
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     134:13338
    Entered STN: 24 Nov 2000
ED
    Long lasting insulinotropic peptides
ΤI
     Bridon, Dominique P.; L'Archeveque, Benoit; Ezrin, Alan M.; Holmes, Darren
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     L.; Leblanc, Anouk; St. Pierre, Serge
     Conjuchem, Inc., Can.
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     PCT Int. Appl., 96 pp.
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    Modified insulinotropic peptides are disclosed. The modified
AB
     insulinotropic peptides are capable of forming a peptidase stabilized
     insulinotropic peptide. The modified insulinotropic peptides are capable
     of forming covalent bonds with one or more blood components to form a
     conjugate. The conjugates may be formed in vivo or ex vivo. The modified
     peptides are administered to treat humans with diabetes and other related
     diseases.
ST
     insulinotropic peptide prepn blood covalent bond; antidiabetic
     insulinotropic peptide
     Sulfhydryl group
ΙT
        (blood protein; long lasting insulinotropic peptides with antidiabetic
        activity)
ΙT
        (components, covalent bonds; long lasting insulinotropic peptides with
        antidiabetic activity)
ΙT
     Antidiabetic agents
        (long lasting insulinotropic peptides with antidiabetic activity)
ΙT
     Peptides, biological studies
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
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(long lasting insulinotropic peptides with antidiabetic activity)
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(1) Conjuchem Inc; WO 9924074 A 1999 HCAPLUS
(2) Conjuchem Inc; WO 9924075 A 1999 HCAPLUS
(3) Conjuchem Inc; WO 9948536 A 1999 HCAPLUS
(4) Hancock, W; US 5614487 A 1997 HCAPLUS
(5) Pouletty, P; EP 0602290 A 1994 HCAPLUS
(6) Redcell Inc; WO 9510302 A 1995 HCAPLUS
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     ANSWER 5 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
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     Entered STN: 24 Nov 2000
ED
     Protection of endogenous therapeutic peptides from peptidase activity
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             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL
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     EP 2000-932570
                       W
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     WO 2000-IB763
                       W
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     WO 2000-US13576
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     US 2000-657332
                       А3
     A method for protecting a peptide from peptidase activity in vivo, the
AB
     peptide being composed of between 2 and 50 amino acids and having a
     C-terminus and an N-terminus and a C-terminus amino acid and an N-terminus
     amino acid is described. In the first step of the method, the peptide is
     modified by attaching a reactive group to the C-terminus amino acid, to
     the N-terminus amino acid, or to an amino acid located between the
     N-terminus and the C-terminus, such that the modified peptide is capable
     of forming a covalent bond in vivo with a reactive functionality on a
     blood component. The solid phase peptide synthesis of a number of derivs.
     with 3-maleimidopropionic acid (3-MPA) is described. In the next step, a
     covalent bond is formed between the reactive group and a reactive
     functionality on a blood component to form a peptide-blood component
     conjugate, thereby protecting said peptide from peptidase activity.
     final step of the method involves the analyzing of the stability of the
     peptide-blood component conjugate to assess the protection of the peptide
     from peptidase activity. Thus, the percentage of a K5 kringle peptide
     (Pro-Arg-Lys-Leu-Tyr-Asp-Lys-NH2) conjugated to human serum albumin via
     MPA remained relatively constant through a 24-h plasma assay in contrast to
     unmodified K5 which decreased to 9% of the original amount of K5 in only 4 h
     in plasma.
     therapeutic peptide conjugation blood albumin stability; peptidase
ST
     stability therapeutic peptide conjugate blood; maleimido conjugation
     therapeutic peptide peptidase stability
TT
     Proteins, specific or class
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
     (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
     PREP (Preparation); PROC (Process); USES (Uses)
        (CART (cocaine and amphetamine-regulated transcript); protection of
        endogenous therapeutic peptides from peptidase activity through
        conjugation to blood components)
IT
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Proteins, specific or class

RL: BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)

(apoptosis-regulating; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

IT Proteins, general, biological studies

RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(blood, conjugates; protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components)

Peptides, biological studies TT

RL: BPR (Biological process); BSU (Biological study, unclassified); SPN

```
(Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
         (conjugates, therapeutic; protection of endogenous therapeutic peptides
        from peptidase activity through conjugation to blood components)
     Fibrinogen degradation products
IT
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
         (fibrinopeptides; protection of endogenous therapeutic peptides from
        peptidase activity through conjugation to blood components)
IT
     Fibronectins
     Laminins
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
     (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
     PREP (Preparation); PROC (Process); USES (Uses)
         (fragments; protection of endogenous therapeutic peptides from
        peptidase activity through conjugation to blood components)
IT
     Complement
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
     (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
     PREP (Preparation); PROC (Process); USES (Uses)
         (inhibitors; protection of endogenous therapeutic peptides from
        peptidase activity through conjugation to blood components)
ΙT
     Functional groups
         (maleimido or succinimidyl; protection of endogenous therapeutic
        peptides from peptidase activity through conjugation to blood
         components)
     Solid phase synthesis
IT
         (peptide; protection of endogenous therapeutic peptides from peptidase
         activity through conjugation to blood components)
     Antimicrobial agents
IT
     Antioxidants
     Signal transduction, biological
         (peptides; protection of endogenous therapeutic peptides from peptidase
         activity through conjugation to blood components)
     Cell adhesion molecules
IT
     Chemotactic factors
     G proteins (guanine nucleotide-binding proteins)
     Gastrointestinal hormones
     Hypothalamic hormones
     Interleukin receptors
     Interleukins
     Osteocalcins
     Pancreatic hormones
     Pituitary hormones
     Tachykinins
     Thyroid hormones
     Toxins
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
      (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
      PREP (Preparation); PROC (Process); USES (Uses)
         (protection of endogenous therapeutic peptides from peptidase activity
         through conjugation to blood components)
     Albumins, biological studies
      RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological
      study); PREP (Preparation); USES (Uses)
         (serum, conjugates; protection of endogenous therapeutic peptides from
         peptidase activity through conjugation to blood components)
      Amyloid
      RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
      (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
      PREP (Preparation); PROC (Process); USES (Uses)
         (\beta-, fragments; protection of endogenous therapeutic peptides from
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peptidase activity through conjugation to blood components)
ΤT
    124219-00-7
    RL: PRP (Properties)
        (Unclaimed; protection of endogenous therapeutic peptides from
       peptidase activity through conjugation to blood components)
IT
     169494-85-3P, Leptin
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
     (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
     PREP (Preparation); PROC (Process); USES (Uses)
        (fragments; protection of endogenous therapeutic peptides from
       peptidase activity through conjugation to blood components)
ΙT
     9002-04-4P, Thrombin
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
     (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
     PREP (Preparation); PROC (Process); USES (Uses)
        (inhibitors; protection of endogenous therapeutic peptides from
        peptidase activity through conjugation to blood components)
     9031-96-3, Peptidase
ΙT
     RL: BAC (Biological activity or effector, except adverse); BSU (Biological
     study, unclassified); BIOL (Biological study)
        (protection of endogenous therapeutic peptides from peptidase activity
        through conjugation to blood components)
     50-56-6P, Oxytocin, biological studies 1393-25-5P, Secretin
IT
     1407-47-2P, Angiotensin 9002-60-2P, ACTH, biological studies
     9002-64-6P, Parathyroid hormone 9002-72-6P, Growth hormone
                                                                  9002-76-02,
             9002-79-3P, MSH 9004-10-8P, Insulin, biological studies
     9007-12-9P, Calcitonin 9007-92-5P, Glucagon, biological studies
     9011-97-6P, Cholecystokinin 9015-71-8P, Corticotropin-releasing factor
     9034-39-3P, Growth hormone-releasing factor 9034-40-6P, Luteinizing
     hormone-releasing factor 9035-81-8P, Trypsin inhibitor
                                                              9088-07-7P,
     Natriuretic peptide 11000-17-2P, Vasopressin
                                                    24305-27-9P,
     Thyrotropin-releasing hormone
                                   31362-50-2P, Bombesin
                                                           37221-79-7P,
     Vasoactive intestinal polypeptide 38916-34-6P, Somatostatin
     39362-14-6P, Prolactin-releasing factor 52906-92-0P, Motilin
     57285-09-3P, Inhibin 58391-28-9P, Leukokinins 59763-91-6P, Pancreatic
                  64190-70-1P, FMRFamide 73019-95-1P, Egg-laying hormone
     polypeptide
     80043-53-4P, Gastrin-releasing peptide 81858-94-8P, Peptide YY (swine)
     82785-45-3P, Neuropeptide Y 83652-28-2P, Calcitonin gene related peptide
     85637-73-6P, Atrial natriuretic peptide 103370-86-1P, Parathormone-like
             106602-62-4P, Amylin 107666-54-6P, Gonadotropin-releasing
     peptide
     hormone-associated peptide 114471-18-0P, Brain natriuretic peptide
     116110-78-2P, Insulin-like peptide 117148-67-1P, Pancreastatin
     119418-04-1P, Galanin 127830-04-0P, C-Type natriuretic peptide
     137061-48-4P, Pituitary adenylate cyclase-activating polypeptide
                            164252-35-1P, Uroguanylin
     144940-98-7P, Guanylin
                 245359-74-4P, Orexin
     Cortistatin
     RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
     (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
     PREP (Preparation); PROC (Process); USES (Uses)
        (protection of endogenous therapeutic peptides from peptidase activity
        through conjugation to blood components;
                                      7423-55-4, 3-Maleimidopropionic acid
ΙT
     6066-82-6, N-Hydroxysuccinimide
     82436-78-0, N-Hydroxysulfosuccinimide
     RL: RCT (Reactant); RACT (Reactant or reagent)
        (protection of endogenous therapeutic peptides from peptidase activity
        through conjugation to blood components)
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                                                                307314-48-3P
ΙT
     224785-55-1P
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IT

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IT

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RL: RCT (Reactant); SPN (Synthetic preparation); THU (Therapeutic use);
BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent);
USES (Uses)
   (protection of endogenous therapeutic peptides from peptidase activity
   through conjugation to blood components)
307315-20-4DP, conjugate with human serum albumin
RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological
study); PREP (Preparation); USES (Uses)
   (protection of endogenous therapeutic peptides from peptidase activity
   through conjugation to blood components)
9015-94-5P, Renin, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); SPN
(Synthetic preparation); THU (Therapeutic use); BIOL (Biological study);
PREP (Preparation); PROC (Process); USES (Uses)
   (substrates and inhibitors; protection of endogenous therapeutic
  peptides from peptidase activity through conjugation to blood
  components)
11063-17-5, Gastric inhibitory polypeptide (swine major)
                                                           12279-41-3,
\alpha1-39-Corticotropin (human)
                             51257-86-4
                                          52232-67-4
                                                        68563-24-6,
Corticotropin-inhibiting peptide (human)
                                           75718-92-2, Peptide F (cattle
                   77465-10-2, \alpha1-39-Corticotropin (rat)
adrenal medulla)
82707-63-9
             83328-95-4, Dynorphin-32 (swine)
1-40-Somatoliberin (human pancreatic islet)
                                              84136-38-9,
1-37-Somatoliberin (human pancreatic islet)
                                            85568-24-7,
1-44-Parathormone (human) 86472-71-1, Somatoliberin (rat hypothalamus)
86546-19-2
             87713-86-8, Peptide B (cattle adrenal medulla)
Glucagon-like peptide I (human)
                                 88402-03-3, Defensin NP 3A (rabbit
          89492-47-7
                        89747-89-7, Transforming growth factor \alpha
(rat reduced)
                90599-39-6
                             90880-43-6
                                          92879-83-9, \alpha-Inhibin-31
                         96351-01-8 96827-07-5
                                                   98226-75-6 98614-76-7
(human seminal plasma)
                                              99658-03-4
99120-49-7, Glucagon-like peptide II (human)
                                                            99658-10-3
100040-31-1, Gastric inhibitory polypeptide (human)
                                                     100915-92-2
            107761-42-2, Glycopeptide (human clone 9-110 amyloid A4
101178-74-9
peptide moiety)
                  110616-04-1
                              111274-30-7, Pancreatic polypeptide (Canis
            111366-38-2
                           112199-06-1
familiaris)
                                          112540-82-6
                                                        112602-83-2,
                      112938-42-8
                                    116977-48-1, Defensin NP 4 (human
Somatoliberin (carp)
          118277-01-3 118337-11-4, Echistatin \alpha1 (reduced)
             120298-73-9
119977-20-7
                            121181-17-7, Glucagon-like peptide 1 (Octodon
        122931-92-4 123337-90-6, Brain natriuretic peptide-45 (rat
degus)
         123757-43-7 124147-28-0, Lymphokine CINC (rat subunit
reduced)
          124541-50-0
                         124834-82-8
                                      124834-83-9
                                                    125199-49-7,
reduced)
Somatoliberin (mouse)
                        126466-47-5
                                      126466-48-6
                                                    127609-05-6
128906-76-3, Decorsin (reduced)
                                 129405-61-4
                                               131438-74-9
                                                              131438-79-4
                           134710-25-1, Calciseptin (Dendroaspis
134090-87-2
             134500-80-4
                              135842-15-8
                                            136751-54-7, C-Type
polylepis polylepis reduced)
natriuretic peptide (human clone \lambda h CNP 53-amino acid isoform
           137467-72-2, C-Type natriuretic peptide (swine clone
reduced)
\lambdaCNP6 53-amino acid isoform reduced)
                                     138634-59-0
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                                                        144409-99-4
141983-93-9
144855-49-2
              146103-03-9
                           148846-98-4, Brain natriuretic peptide-45
(mouse reduced)
                  150679-91-7
                                150680-28-7, Adrenomedullin (human clone
pHAM-3)
         150871-76-4
                      151247-82-4, Margatoxin (reduced)
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155420-59-0
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161247-48-9
                             161818-07-1, Endothelin 3 (rat reduced)
              161278-54-2
161247-61-6
164714-89-0, \omega-Agatoxin TK 2 (reduced)
                                        165168-50-3, Toxin ShK
                                                     166090-74-0
(Stoichactis helianthus potassium-channel reduced)
              171543-83-2, Urocortin (Rattus norvegicus)
                                                             173010-28-1,
166798-69-2
            174394-41-3 175524-68-2, Glucagon-like peptide 1 (Amphiuma
Buforin I
               175779-77-8, Glucagon-like peptide 2 (Amphiuma tridactylum)
tridactylum)
                                           183681-18-7
                                                          184007-69-0
                             183598-56-3
179733-43-8
              179733-44-9
                                           186673-14-3
                                                          186673-15-4
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              186673-12-1
186322-91-8
              186673-17-6
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186673-16-5
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                             187111-84-8
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186673-21-2
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309260-75-1
RL: PRP (Properties)
   (unclaimed protein sequence; protection of endogenous therapeutic
   peptides from peptidase activity through conjugation to blood
   components)
                                                          309262-14-4
                                           309262-13-3
309260-78-4
              309260-79-5
                             309260-80-8
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RL: PRP (Properties)
   (unclaimed protein sequence; protection of endogenous therapeutic
   peptides from peptidase activity through conjugation to blood
   components)
53-73-6
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                                484-43-5
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                                                        4086-29-7
          58-49-1
                                             7266-47-9.
            5576-42-1, α1-16-Corticotropin
4474-91-3
                                   9072-41-7, Motilin (swine)
                      9063-57-4
\alpha1-17-Corticotropin
             13602-53-4
                          16322-68-2
                                        16376-83-3
                                                     16941-32-5, Glucagon
10587-93-6
                                             17908-57-5.
         16960-16-0, \alpha 1-24-Corticotropin
\beta-Melanotropin (human) 19941-13-0, \beta-Melanotropin (swine)
             22006-64-0, \alpha1-13-Corticotropin
                                                23025-68-5
20845-02-7
25422-31-5, Fibrinopeptide A (human)
                                        26251-06-9
                                                      32204-93-6
             33017-11-7, Proinsulin C-peptide (human)
                                                          33512-65-1,
32222-04-1
                      34233-50-6 35144-91-3
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α6-24-Corticotropin
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IT

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    2000:493318 HCAPLUS
    133:129880
    Entered STN:
                   21 Jul 2000
    Methods using an exendin or related substance for glucagon suppression
    Young, Andrew; Gedulin, Bronislava
    Amylin Pharmaceuticals, Inc., USA
    PCT Int. Appl., 96 pp.
    CODEN: PIXXD2
    Patent
    English
    A61K038-26
    1-10 (Pharmacology)
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                            20000110
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    WO 2000-US942
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    Methods are provided for use of an exendin, an exendin agonist, or a
     modified exendin or exendin agonist having an exendin or exendin agonist
     linked to one or more polyethylene glycol polymers, for example, for
     lowering glucagon levels and/or suppressing glucagon secretion in a
     subject. These methods are useful in treating hyperglucagonemia and other
     conditions that would be benefited by lowering plasma glucagon or
     suppressing glucagon secretion.
     exendin glucagon suppression; hyperglucagonemia glucagon suppression
     exendin
     Kidney
        (clearance by; exendin or related substance for glucagon suppression)
     Polyoxyalkylenes, biological studies
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RL: BAC (Biological activity or effector, except adverse); BSU (Biological
    study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
     (Uses)
        (exendin conjugates; exendin or related substance for glucagon
       suppression)
    Antidiabetic agents
    Gastric emptying
        (exendin or related substance for glucagon suppression)
    Pancreatic islet of Langerhans
    Pancreatic islet of Langerhans
        (glucagonoma, inhibitors; exendin or related substance for glucagon
        suppression)
    Antitumor agents
        (glucagonoma; exendin or related substance for glucagon suppression)
    Erythema
        (necrolytic migratory; exendin or related substance for glucagon
        suppression)
    Diabetes mellitus
        (non-insulin-dependent; exendin or related substance for glucagon
        suppression)
    130357-25-4P, Exendin 3 (Heloderma horridum)
                                                    141758-74-9P, Exendin 4
     (Heloderma suspectum)
    RL: BAC (Biological activity or effector, except adverse); BSU (Biological
    study, unclassified); PRP (Properties); SPN (Synthetic preparation); THU
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    25322-68-3D, Polyethylene glycol, exendin conjugates
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     50-99-7, D-Glucose, biological studies
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        (unclaimed sequence; methods using an exendin or related substance for
        glucagon suppression)
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     2000:493315 HCAPLUS
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     133:135612
     Entered STN: 21 Jul 2000
ED
TI
     Novel exendin agonist formulations and methods of administration thereof
     Young, Andrew; L'Italien, James J.; Kolterman, Orville
IN
PΑ
     Amylin Pharmaceuticals, Inc., USA
SO
     PCT Int. Appl., 281 pp.
     CODEN: PIXXD2
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     English
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     A61K038-16
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     34-3 (Amino Acids, Peptides, and Proteins)
     Section cross-reference(s): 2, 63
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US 2000-175365P

WO 2000-US902 W 20000114 US 2001-889330 A2 20011227

- AB Novel exendin and exendin agonist compound formulations and dosages and methods of administration thereof are provided. These compns. and methods are useful in treating diabetes and conditions that would be benefited by lowering plasma glucose or delaying and/or slowing gastric emptying or inhibiting food intake.
- ST exendin agonist antidiabetic sequence appetite suppressant

IT Glucagon-like peptide-1 receptors

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(GLP-1; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Buffers

(acetate; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Drug delivery systems

(buccal; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Phosphates, uses

RL: NUU (Other use, unclassified); USES (Uses)
(buffers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Stomach

(emptying of; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Drug delivery systems

(freeze-dried; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Drug delivery systems

(injections, s.c.; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Drug delivery systems

(injections; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Drug delivery systems

(intratracheal; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Polyoxyalkylenes, uses

RL: NUU (Other use, unclassified); USES (Uses)
(iso-osmolality modifier; novel exendin agonist formulations and
methods of administration thereof as antidiabetic agents and appetite
suppressants)

IT Solutions

(isotonic solns.; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Drug delivery systems

(liqs.; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite suppressants)

IT Osmolality

(modifiers; novel exendin agonist formulations and methods of administration thereof as antidiabetic agents and appetite

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suppressants)
    Drug delivery systems
IT
        (nasal; novel exendin agonist formulations and methods of
        administration thereof as antidiabetic agents and appetite
        suppressants)
TT
    Diabetes mellitus
        (non-insulin-dependent; novel exendin agonist formulations and methods
        of administration thereof as antidiabetic agents and appetite
ΙT
     Detergents
        (nonionic; novel exendin agonist formulations and methods of
        administration thereof as antidiabetic agents and appetite
        suppressants)
    Antidiabetic agents
TT
    Appetite depressants
     Heloderma horridum
     Heloderma suspectum
     Obesity
     Physiological saline solutions
     Preservatives
     Protein sequences
     Surfactants
     Thickening agents
        (novel exendin agonist formulations and methods of administration
        thereof as antidiabetic agents and appetite suppressants)
     Peptides, preparation
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        (novel exendin agonist formulations and methods of administration
        thereof as antidiabetic agents and appetite suppressants)
     Drug delivery systems
TΤ
        (oral; novel exendin agonist formulations and methods of administration
        thereof as antidiabetic agents and appetite suppressants)
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        (parenterals; novel exendin agonist formulations and methods of
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        suppressants)
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     Alcohols, uses
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        (polyhydric, iso-osmolality modifiers; novel exendin agonist
        formulations and methods of administration thereof as antidiabetic
        agents and appetite suppressants)
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        (pulmonary; novel exendin agonist formulations and methods of
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study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
   (amino acid sequence; novel exendin agonist formulations and methods of
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50-99-7, D-Glucose, biological studies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified);
BIOL (Biological study); OCCU (Occurrence)
   (blood; novel exendin agonist formulations and methods of
   administration thereof as antidiabetic agents and appetite
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126-44-3, Citrate, uses 11070-68-1, Glutamate, uses
RL: NUU (Other use, unclassified); USES (Uses)
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71-50-1, Acetate, properties
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   (buffers; novel exendin agonist formulations and methods of
   administration thereof as antidiabetic agents and appetite
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50-70-4, Sorbitol, uses 56-81-5, 1,2,3-Propanetriol, uses 59-23-4,
Galactose, uses 69-65-8, Mannitol 87-89-8, Inositol 87-99-0, Xylitol
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89750-14-1, Glucagon-like peptide I
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     9004-10-8, Insulin, biological studies
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L30
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AN
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     Entered STN: 31 Aug 1998
ED
     Polynucleotides encoding proexendin, and methods and uses thereof
ΤI
     Drucker, Daniel J.
ΙN
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     1149336 Ontario Inc., Can.
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     CODEN: PIXXD2
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AΒ
     Exendin 4 is a biol. active peptide first isolated from Gila monster
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The invention encompasses polynucleotides encoding proexendin peptides, including exendin and novel peptides, as well as isolated or recombinant proexendin peptides. The invention also includes antibodies which specifically recognize such peptides. Heloderma proexendin sequence immunity insulinotropic diabetes STImmunity IT (administration of peptides for immunity; gene encoding proexendin from Heloderma horridum and applications) Heloderma horridum ΙT Protein sequences (gene encoding proexendin from Heloderma horridum and applications) TΤ Antibodies RL: ARU (Analytical role, unclassified); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study) (gene encoding proexendin from Heloderma horridum and applications) IT Diabetes mellitus (non-insulin-dependent, insulinotropic GLP-1 like properties of exendin with applications for treatment of diabetes; gene encoding proexendin from Heloderma horridum and applications) IT 141732-76-5, Exendin 4 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (alternative form of;; gene encoding proexendin from Heloderma horridum and applications) 211430-73-8, Exendin ENTP (Heloderma horridum) ΙT RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (amino acid sequence of mature; gene encoding proexendin from Heloderma horridum and applications) 188265-76-1, Exendin 4, pro- (Heloderma suspectum) ΙT 203743-40-2 211319-02-7 211319-03-8 **211430-62-5** 211319-01-6 211430-68-1, 1-47-Exendin ENTP (Heloderma horridum) RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (amino acid sequence; gene encoding proexendin from Heloderma horridum and applications) 89750-14-1, Glucagon-like peptide I IT RL: BSU (Biological study, unclassified); BIOL (Biological study) (insulinotropic GLP-1 like properties of exendin with applications for treatment of diabetes; gene encoding proexendin from Heloderma horridum and applications) ΙT 211621-97-5 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (nucleotide sequence; gene encoding proexendin from Heloderma horridum and applications) THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD RE.CNT (1) Chen, Y; THE JOURNAL OF BIOLOGICAL CHEMISTRY 1997, V272(7), P4108 HCAPLUS (2) Eng, J; US 5424286 A 1995 HCAPLUS (3) Eng, J; JOURNAL OF BIOLOGICAL CHEMISTRY 1992, V267(11), P7402 HCAPLUS (4) Pohl, M; GASTROENTEROLOGY, SUPPLEMENT 1997, V112(4), PA1181 L30 ANSWER 9 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN 1998:490528 HCAPLUS AN DN 129:149256 Entered STN: 06 Aug 1998 ED Preparation of exendin peptides for the reduction of food intake TΙ Beeley, Nigel Robert Arnold; Prickett, Kathryn S.; Bhavsar, Sunil INAmylin Pharmaceuticals, Inc., USA PΑ PCT Int. Appl., 214 pp. SO CODEN: PIXXD2

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Patent

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LA
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     Methods for treating conditions or disorders which can be alleviated by
AΒ
     reducing food intake are disclosed which comprise administration of an
     effective amount of an exendin or an exendin agonist, alone or in
     conjunction with other compds. or compns. that effect satiety. Approx.
     180 exendin-related peptides were synthesized by the solid-phase method.
ST
     exendin peptide prepn redn food intake
ΙT
     Appetite
        (disorder; preparation of exendin peptides for the reduction of food intake)
IT
     Appetite depressants
     Feeding
        (preparation of exendin peptides for the reduction of food intake)
ΙT
     Peptides, preparation
     RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological
     study); PREP (Preparation); USES (Uses)
        (preparation of exendin peptides for the reduction of food intake)
TT
     210712-52-0P
     RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological
     study); PREP (Preparation); USES (Uses)
        (.preparation of exendin peptides for the reduction of food intake)
     158345-16-5P 203743-29-7P 203743-31-1P
TT
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     203743-50-4P 203743-53-7P 203743-54-8P 210712-28-0P, 1-30-Exendin 4 (Heloderma suspectum) 210712-29-1P 210712-30-4P
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     RL: FFD (Food or feed use); SPN (Synthetic preparation); BIOL (Biological
     study); PREP (Preparation); USES (Uses)
        (preparation of exendin peptides for the reduction of food intake)
            THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
RE
(1) Eng; US 5424286 A 1995 HCAPLUS
     ANSWER 10 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
     1998:112250 HCAPLUS
ΑN
     128:192936
DN
     Entered STN: 25 Feb 1998
ED
     Preparation of exendin peptide analogs as agonists for regulating
TI
     gastrointestinal motility
     Young, Andrew A.; Gedulin, Bronislava; Beeley, Nigel
IN
     Robert Arnold; Prickett, Kathryn S.
     Amylin Pharmaceuticals, Inc., USA; Young, Andrew A.; Gedulin,
PΑ
     Bronislava; Beeley, Nigel Robert Arnold; Prickett, Kathryn S.
     PCT Int. Appl., 70 pp.
SO
     CODEN: PIXXD2
DT
     Patent
     English
T.A
     ICM A61K038-00
IC
     ICS A61K038-26; G03F005-00; C07K002-00; C07K005-00
     34-3 (Amino Acids, Peptides, and Proteins)
CC
     Section cross-reference(s): 1
FAN.CNT 1
                                            APPLICATION NO. DATE
                      KIND DATE
     PATENT NO.
                                              _____
     ______
     WO 9805351 A1 19980212 WO 1997-US14199 19970808 <--
PΤ
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          VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA,
              GN, ML, MR, NE, SN, TD, TG
                                                                19970808 <--
     AU 9740636 A1 19980225
                                              AU 1997-40636
                                             EP 1997-938261 19970808 <--
                            19991229
                        A1
      EP 966297
          R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, FI
                        Т2
                                              JP 1998-508263 19970808 <--
                              20010206
      JP 2001501593
PRAI US 1996-694954 A
WO 1997-US14199 W
                              19960808 <--
                              19970808 <--
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OS MARPAT 128:192936 Methods for reducing gastric motility and delaying gastric emptying for AB therapeutic and diagnostic purposes are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist H-Xaal-Xaa2-Xaa3-Gly-Thr-Xaa4-Xaa5-Xaa6-Xaa7-Xaa8-Ser-Lys-Gln-Xaa9-Glu-Glu-Glu-Ala-Val-Arg-Leu-Xaa10-Xaa11-Xaa12-Xaa13-Leu-Lys-Asn-Gly-Gly-Xaa14-Ser-Ser-Gly-Ala-Xaa15-Xaa16-Xaa17-Xaa18-Z [Xaal = His, Arg, Tyr; Xaa2 = Ser, Gly, Ala, Thr; Xaa3, Xaa7, Xaa12 = independently Asp, Glu; Xaa4, Xaa10 = independently Phe, Tyr, naphthylalanine; Xaa5, Xaa6 = independently Thr, Ser; Xaa8, Xaa9 = independently Leu, Ile, Val, pentylglycine, Met; Xaall = any group Xaa8, tert-butylglycine; Xaa13 = any group Xaa4, Trp; Xaa14-Xaa17 = independently Pro, homoproline, 3-Hyp, 4-Hyp, thioproline, N-alkylglycine, N-alkylpentylglycine, N-alkylalanine; Xaa18 = Ser, Thr, Tyr; Z = OH, NH2; with the proviso that the compound does not have the formula of exendin-3 or exendin-4] or a pharmaceutically acceptable salt thereof. Methods for treating conditions associated with elevated, inappropriate, or undesired post-prandial blood glucose levels are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist alone or in conjunction with other anti-gastric emptying agents. Thus, exendin-4 acid and [Leul4, Phe25]-exendin-4, prepared by standard solid-phase methods on a 4-(2,4-dimethoxyphenyl)-Fmocaminomethylphenoxyacetamide norleucine-MBHA resin using 9-fluorenylmethoxycarbonyl (Fmoc)-protected amino acids, inhibited gastric emptying in male HSD rats with EC50 = 0.12 and 0.29 μg . Exendin-4 showed EC50 = 0.27 μg under the same conditions. exendin analog prepn gastrointestinal motility antagonist; gastric STemptying antagonist exendin analog prepn; antidiabetic agent exendin analog prepn Antidiabetic agents ΙT Gastric emptying Gastrointestinal motility (preparation of exendin peptide analogs as agonists for regulating gastrointestinal motility) 107444-51-9P, Glucagon-like peptide-I(7-36) amide 130357-25-4P, TT Exendin-3 (Heloderma horridum) 133514-43-9P, Exendin[9-39] 141758-74-9P, Exendin-4 (Heloderma suspectum) 158345-16-5P 203743-26-4P 203743-27-5P 203743-28-6P 203743-30-0P 203743-31-1P 203743-29-7P 203743-32-2P 203743-33-3P 203743-35-5P 203743-36-6P 203743-37-7P 203743-38-8P 203743-40-2P **203743-41-3P** 203743-42-4P 203743-39-9P 203743-43-5P 203743-44-6P 203743-45-7P 203743-46-8P 203743-47-9P 203743-49-1P 203743-48-0P 203743-50-4P 203743-51-5P 203743-52-6P 203743-53-7P 203743-54-8P 203743-55-9P RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (preparation of exendin peptide analogs as agonists for regulating gastrointestinal motility) THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD RE.CNT (1) Amylin Pharmaceuticals Inc; WO 9507098 1995 (2) Bayer; Clinical Chemistry 1996, V42(8B), P1361 (3) Chernish; US 3862301 A 1973 HCAPLUS (4) Daniel; Br Med J 1974, V3, P720 MEDLINE (5) Dupre; Diabetes 1995, V44(6), P626 HCAPLUS (6) D'Alessio; J Clin Invest 1994, V93(5), P2263 HCAPLUS (7) Hellstrom; Scand J Gastroenterol 1993, V28(Suppl 197), P38 (8) Miholic; Chirurgisches Forum 1991, P429 HCAPLUS (9) Nauck; Diabetologia, Abstract No 148 1995, V38(Suppl 1), PA39 (10) Rai; Am Physiol J 1993, V265, PG118 MEDLINE

(11) Schirra; Gastroenterology 1995, V108(4), PA1003

- (12) Schirra; Proceedings of the Association of American Physicians 1997, V109(1), P84 HCAPLUS
- L30 ANSWER 11 OF 11 HCAPLUS COPYRIGHT 2003 ACS on STN
- AN 1994:622490 HCAPLUS
- DN 121:222490
- ED Entered STN: 12 Nov 1994
- TI Use of 125I-[Y39]exendin-4 to characterize exendin receptors on dispersed pancreatic acini and gastric chief cells from guinea pig
- AU Singh, Gurcharn; Eng, John; Raufman, Jean-Pierre
- CS Gastrointestinal Cell Biology Laboratory, State University of New York-Health Science Center at Brooklyn, 450 Clarkson Avenue-Box 1196, Brooklyn, NY, 11203-2098, USA
- SO Regulatory Peptides (1994), 53(1), 47-59 CODEN: REPPDY; ISSN: 0167-0115
- DT Journal
- LA English
- CC 2-6 (Mammalian Hormones)
- We synthesized and iodinated an exendin-4 analog, [Y39]exendin-4 (700 AΒ Ci/mmol), for use as a radioligand to characterize exendin receptors on dispersed pancreatic acini and gastric chief cells from guinea pig. Binding of this bioactive radioligand was rapid, temperature-dependent and specific (not inhibited by other pancreatic or gastric secretagogues). Measurement of the ability of exendin-4 to inhibit the binding of 125I-[Y39]exendin-4 indicated the presence of two classes of receptors. Pancreatic acini had 12.5 + 1010 binding sites/mg acinar protein of which 6% were high affinity (Kd = 0.5 nM) and 94% were low affinity (Kd = 0.1 μ M). Chief cells had 3370 binding sites/cell of which 9% were high affinity (Kd = 0.3 nM) and 91% were low affinity (Kd = 0.2 μ M). Washing with 0.2 M acetic acid (pH 2.5), 0.2 M glycine (pH 10.5), or trypsin (100 μ g/mL) after 30 min incubation at 37°, indicated that 63 and 49% of radioligand was internalized in acini and chief cells, resp. Truncated glucagon-like peptide-1 (tGLP-1), a mammalian peptide sharing 53% homol. with exendin-4, inhibited radioligand binding at the same concns. that altered secretion from acini and chief cells. Glucagon, GLP-1 and GLP-2 inhibited 125I-[Y39]exendin-4 binding only at concns. ≥100 nM. Exendin(9-39)NH2, a specific exendin-receptor antagonist, potently inhibited 125I-[Y39] exendin-4 binding (IC50 = 6.1 and 3.5 nM in acini and chief cells, resp.). In pancreatic acini and gastric chief cells from guinea pig, exendin-3, exendin-4 and tGLP-1 increase cellular cAMP and modulate enzyme secretion by interacting with high-affinity exendin receptors. 125I-[Y39] exendin-4 is a useful radioligand for studying exendin receptors.
- ST exendin receptor pancreas stomach
- IT Enzymes

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(exendins modulation of pancreas acinus and stomach chief cell secretion of)

IT Pancreas

(acinus, exendin receptors of)

IT Stomach

(chief cell, exendin receptors of)

IT Receptors

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(exendin, of pancreas acini and stomach chief cells)

IT 118549-37-4, Insulinotropin 130357-25-4, Exendin 3 (Heloderma horridum) 141758-74-9

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)

(cAMP formation and enzyme secretion by pancreas acinus and stomach

- 7

chief cells response to) TT 60-92-4, CAMP RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process) (exendins modulation of pancreas acinus and stomach chief cell formation of) ΙT 158345-16-5P RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent) (preparation and radioiodination of) 158345-15-4P 158345-17-6P IT RL: SPN (Synthetic preparation); PREP (Preparation) (preparation as radioligand for extendin receptors) => fil uspatall FILE 'USPATFULL' ENTERED AT 10:17:55 ON 29 DEC 2003 CA INDEXING COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS) FILE 'USPAT2' ENTERED AT 10:17:55 ON 29 DEC 2003 CA INDEXING COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS) => d bib abs hitrn tot 131 L31 ANSWER 1 OF 11 USPATFULL on STN 2003:158955 USPATFULL AN Long lasting synthetic glucagon-like peptide {GLP-1} TΤ Bridon, Dominique P., Outremont, CANADA TN L' Archeveque, Benoit, Laval, CANADA Ezrin, Alan M., Moraga, CA, UNITED STATES Holmes, Darren L., Montreal, CANADA Leblanc, Anouk, Montreal, CANADA Pierre, Serge St., Ile Bizard, CANADA 20030612 Α1 PΙ US 2003108568 20021104 (10) A1 US 2002-288340 ΑI Division of Ser. No. US 2000-657332, filed on 7 Sep 2000, GRANTED, Pat. RLI No. US 6514500 19991015 (60) US 1999-159783P PRAI DT Utility APPLICATION FS Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San LREP Francisco, CA, 94105-2482 Number of Claims: 19 CLMN Exemplary Claim: 1 ECLNo Drawings DRWN LN.CNT 2344 CAS INDEXING IS AVAILABLE FOR THIS PATENT. Modified insulinotropic peptides are disclosed. The modified AB insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases. CAS INDEXING IS AVAILABLE FOR THIS PATENT. 309729-73-5 TT (lasting insulinotropic pepwith antidiabetic activity) 308245-55-8 308806-01-1 308815-99-8 ΙT (long lasting insulinotropic peptides with antidiabetic activity) 308244-92-0P 308249-19-6P 309728-25-4P TΥ 309729-78-0P 309729-82-6P

(long lasting insulinotropic peptides with antidiabetic activity)

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L31 ANSWER 2 OF 11 USPATFULL on STN
       2003:158954 USPATFULL
ΑN
       Long lasting synthetic glucagon-like peptide {GLP-1}
ΤI
       Bridon, Dominique P., Outremont, CANADA
IN
       L'Archeveque, Benoit, Laval, CANADA
       Ezrin, Alan M., Moraga, CA, UNITED STATES
       Holmes, Darren L., Montreal, CANADA
       Leblanc, Anouk, Montreal, CANADA
       St. Pierre, Serge, Ile Bizard, CANADA
                          Α1
                               20030612
       US 2003108567
PΙ
                               20021104 (10)
                          Α1
       US 2002-287892
ΑI
       Division of Ser. No. US 2000-657332, filed on 7 Sep 2000, GRANTED, Pat.
RLI
       No. US 6514500
                           19991015 (60)
       US 1999-159783P
PRAI
\mathsf{DT}
       Utility
       APPLICATION
FS
       Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San
LREP
       Francisco, CA, 94105-2482
       Number of Claims: 19
CLMN
       Exemplary Claim: 1
ECL
       No Drawings
DRWN
LN.CNT 2359
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
       Modified insulinotropic peptides are disclosed. The modified
AΒ
       insulinotropic peptides are capable of forming a peptidase stabilized
       insulinotropic peptide. The modified insulinotropic peptides are capable
       of forming covalent bonds with one or more blood components to form a
       conjugate. The conjugates may be formed in vivo or ex vivo. The modified
       peptides are administered to treat humans with diabetes and other
       related diseases.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     309729-73-5
IT
         (lasting insulinotropic pepwith antidiabetic activity)
     308245-55-8 308806-01-1 308815-99-8
IT
      309729-80-4
         (long lasting insulinotropic peptides with antidiabetic activity)
     308244-92-0P 308249-19-6P 309728-25-4P
ΙT
      309729-78-0P 309729-82-6P
         (long lasting insulinotropic peptides with antidiabetic activity)
L31 ANSWER 3 OF 11 USPATFULL on STN
       2003:127606 USPATFULL
ΑN
       Exendins, exendin agonists, and methods for their use
TΙ
       Beeley, Nigel Robert Arnold, Solana Beach, CA, UNITED STATES
IN
        Prickett, Kathryn S., San Diego, CA, UNITED STATES
        Bhavsar, Sunil, San Diego, CA, UNITED STATES
                                20030508
PΙ
       US 2003087821
                           Α1
                                20020628 (10)
       US 2002-187051
                           Α1
ΑI
       Continuation of Ser. No. US 1998-3869, filed on 7 Jan 1998, PENDING
RLI
                            19970107 (60)
       US 1997-34905P
PRAT
                            19970808 (60)
       US 1997-55404P
                            19971114 (60)
       US 1997-66029P
                            19971114 (60)
        US 1997-65442P
        Utility
DT
        APPLICATION
FS
        Lisa M. McGeehan, Brobeck, Phleger & Harrison LLP, 12390 El Camino Real,
LREP
        San Diego, CA, 92130-2081
        Number of Claims: 31
CLMN
        Exemplary Claim: 1
 ECL
 DRWN
        10 Drawing Page(s)
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LN.CNT 3914
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
       Methods for treating conditions or disorders which can be alleviated by
       reducing food intake are disclosed which comprise administration of an
       effective amount of an exendin or an exendin agonist, alone or in
       conjunction with other compounds or compositions that affect satiety.
       The methods are useful for treating conditions or disorders, including
       obesity, Type II diabetes, eating disorders, and insulin-resistance
       syndrome. The methods are also useful for lowering the plasma glucose
       level, lowering the plasma lipid level, reducing the cardiac risk,
       reducing the appetite, and reducing the weight of subjects.
       Pharmaceutical compositions for use in the methods of the invention are
       also disclosed.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     158345-16-5P 203743-29-7P 203743-31-1P
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      203743-36-6P 203743-37-7P 203743-38-8P
      203743-39-9P 203743-41-3P 203743-45-7P
      203743-46-8P 203743-47-9P 203743-53-7P
      203743-54-8P 210829-41-7P 210829-46-2P
      210830-02-7P 210830-13-0P 210830-31-2P
      210830-35-6P 210830-59-4P
        (preparation of exendin peptides for the reduction of food intake)
L31 ANSWER 4 OF 11 USPATFULL on STN
       2003:127605 USPATFULL
AN
       Novel exendin agonist formulations and methods of administration thereof
ТT
       Young, Andrew A., La Jolla, CA, UNITED STATES
IN
       Kolterman, Orville G., Poway, CA, UNITED STATES
                          A1
                               20030508
PΙ
       US 2003087820
                          A1
                               20020528 (10)
       US 2002-157224
ΑI
       Continuation-in-part of Ser. No. US 2001-889330, filed on 27 Dec 2001,
RLI
       PENDING A 371 of International Ser. No. WO 2000-US902, filed on 14 Jan
       2000, PENDING
                           19990114 (60)
PRAI
       US 1999-116380P
                           20000110 (60)
       US 2000-175365P
DT
       Utility
FS
       APPLICATION
       Molly A. Holman, Ph.D., Amylin Pharmaceuticals, Inc., 9373 Towne Centre
LREP
       Drive, San Diego, CA, 92121
CLMN
       Number of Claims: 40
ECL
       Exemplary Claim: 1
DRWN
       25 Drawing Page(s)
LN.CNT 3512
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
       Novel exendin and exendin agonist compound formulations and dosages and
       methods of administration thereof are provided. These compositions and
       methods are useful in treating diabetes and conditions that would be
       benefited by lowering plasma glucose or delaying and/or slowing gastric
       emptying or inhibiting food intake.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     522007-08-5 522007-09-6 522007-10-9
      522007-12-1 522007-13-2 522007-15-4
      522007-16-5 522007-17-6 522007-18-7
      522007-24-5 522007-25-6 522007-28-9
      522007-29-0 522007-30-3 522007-31-4
      522007-32-5
```

(unclaimed protein sequence; novel exendin agonist formulations and

L31 ANSWER 5 OF 11 USPATFULL on STN

methods of administration thereof)

```
2003:51546 USPATFULL
AN
       Use of exendins and agonists thereof for modulation of triglyceride
TΙ
       levels and treatment of dyslipidemia
       Kolterman, Orville G., Poway, CA, UNITED STATES Young, Andrew A., Point Loma, CA, UNITED STATES
IN
       Amylin Pharmaceuticals, Inc. (U.S. corporation)
PΑ
                                20030220
       US 2003036504
                           Α1
PΙ
                                20010109 (9)
       US 2001-756690
                           A1
ΑI
                            20000110 (60)
       US 2000-175365P
PRAI
DT
       Utility
FS
       APPLICATION
       BROBECK, PHLEGER & HARRISON LLP, 12390 EL CAMINO REAL, SAN DIEGO, CA,
LREP
       Number of Claims: 40
CLMN
       Exemplary Claim: 1
ECL
       5 Drawing Page(s)
DRWN
LN.CNT 5350
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
       Methods for modulating the levels of plasma triglyceride and other
       lipids in a subject which comprise administration of an effective amount
       of an exendin or an exendin agonist, alone or in conjunction with other
       compounds or compositions that lower blood triglyceride and/or other
       lipid levels.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     284676-24-0
IΤ
         (unclaimed protein sequence; methods using an exendin or related
        substance for glucagon suppression)
L31 ANSWER 6 OF 11 USPATFULL on STN
       2003:33172 USPATFULL
AN
       Long lasting synthetic glucagon like peptide {GLP-!}
TT
       Bridon, Dominique P., Outremont, CANADA
TN
       L'Archeveque, Benoit, Laval, CANADA
       Ezrin, Alan M., Moraga, CA, United States
       Holmes, Darren L., Montreal, CANADA
        Leblanc, Anouk, Montreal, CANADA
        St. Pierre, Serge, Ile Bizard, CANADA
        Conjuchem, Inc., Montreal, CANADA (non-U.S. corporation)
PΑ
PΙ
        US 6514500
                           В1
                                20030204
                                 20000907 (9)
        US 2000-657332
ΑI
                           19991015 (60)
PRAI
       US 1999-159783P
DT
        Utility
FS
        GRANTED
EXNAM Primary Examiner: Housel, James; Assistant Examiner: Lucas, Zachariah
       Morrison & Foerster LLP
LREP
        Number of Claims: 2
CLMN
        Exemplary Claim: 1
ECL
        0 Drawing Figure(s); 0 Drawing Page(s)
DRWN
LN.CNT 2251
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
        Modified insulinotropic peptides are disclosed. The modified
        insulinotropic peptides are capable of forming a peptidase stabilized
        insulinotropic peptide. The modified insulinotropic peptides are capable
        of forming covalent bonds with one or more blood components to form a
        conjugate. The conjugates may be formed in vivo or ex vivo. The modified
        peptides are administered to treat humans with diabetes and other
        related diseases.
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.
 ΙT
      309729-73-5
         (lasting insulinotropic pepwith antidiabetic activity)
```

308245-55-8 308806-01-1 308815-99-8

ΙT

```
309729-80-4
        (long lasting insulinotropic peptides with antidiabetic activity)
     308244-92-0P 308249-19-6P 309728-25-4P
IT
      309729-78-0P 309729-82-6P
        (long lasting insulinotropic peptides with antidiabetic activity)
L31 ANSWER 7 OF 11 USPATFULL on STN
       2003:13287 USPATFULL
ΑN
       Use of exendins and agonists thereof for the treatment of gestational
ΤI
       diabetes mellitus
       Hiles, Richard A., San Diego, CA, United States
IN
       Prickett, Kathryn S., San Diego, CA, United States
       Amylin Pharmaceuticals, Inc., San Diego, CA, United States (U.S.
PA
       corporation)
                          В1
                               20030114
PΙ
       US 6506724
                               19990601 (9)
       US 1999-323867
ΑI
       Utility
DT
FS
       GRANTED
EXNAM Primary Examiner: Celsa, Bennett
       Brobeck, Phleger & Harrison LLP
LREP
       Number of Claims: 13
CLMN
       Exemplary Claim: 1
ECL
       3 Drawing Figure(s); 4 Drawing Page(s)
DRWN
LN.CNT 5263
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
       Methods for treating gestational diabetes which comprise administration
AB
       of an effective amount of an exendin or an exendin agonist, alone or in
       conjunction with other compounds or compositions that lower blood
       glucose levels.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     158345-16-5P 203743-29-7P 203743-31-1P
      203743-32-2P 203743-33-3P 203743-35-5P
      203743-36-6P 203743-37-7P 203743-38-8P
      203743-41-3P 203743-45-7P 203743-46-8P
      203743-47-9P 210830-02-7P 210830-13-0P
      210830-35-6P 210830-59-4P 284676-24-0P
      312932-20-0P 312932-28-8P 312933-83-8P
      312949-21-6P 312949-26-1P
        (use of exendins and agonists thereof for treatment of gestational
        diabetes mellitus in relation to combination with insulin or amylin
        agonist)
L31 ANSWER 8 OF 11 USPATFULL on STN
ΑN
       2002:251713 USPATFULL
       USE OF EXENDINS AND AGONISTS THEREOF FOR THE REDUCTION OF FOOD INTAKE
TΙ
       BEELEY, NIGEL ROBERT ARNOLD, SOLANA BEACH, CA, UNITED STATES
IN
       PRICKETT, KATHRYN S., SAN DIEGO, CA, UNITED STATES
       BHAVSAR, SUNIL, SAN DIEGO, CA, UNITED STATES
                          Α1
                               20020926
PΙ
       US 2002137666
                               19980107 (9)
       US 1998-3869
                          Α1
ΑI
                          19970107 (60)
       US 1997-34905P
PRAI
                           19970808 (60)
       US 1997-55404P
       US 1997-66029P
                           19971114 (60)
                           19971114 (60)
       US 1997-65442P
DT
       Utility
FS
       APPLICATION
       LYON & LYON LLP, 633 WEST FIFTH STREET, SUITE 4700, LOS ANGELES, CA,
LREP
       90071
       Number of Claims: 31
CLMN
       Exemplary Claim: 1
ECL
DRWN
       11 Drawing Page(s)
LN.CNT 3909
```

liu - 09 / 889331 CAS INDEXING IS AVAILABLE FOR THIS PATENT. Methods for treating conditions or disorders which can be alleviated by reducing food intake are disclosed which comprise administration of an effective amount of an exendin or an exendin agonist, alone or in conjunction with other compounds or compositions that affect satiety. The methods are useful for treating conditions or disorders, including obesity, Type II diabetes, eating disorders, and insulin-resistance syndrome. The methods are also useful for lowering the plasma glucose level, lowering the plasma lipid level, reducing the cardiac risk, reducing the appetite, and reducing the weight of subjects. Pharmaceutical compositions for use in the methods of the invention are also disclosed. CAS INDEXING IS AVAILABLE FOR THIS PATENT. 158345-16-5P 203743-29-7P 203743-31-1P 203743-32-2P 203743-33-3P 203743-35-5P 203743-36-6P 203743-37-7P 203743-38-8P 203743-39-9P 203743-41-3P 203743-45-7P 203743-46-8P 203743-47-9P 203743-53-7P 203743-54-8P 210829-41-7P 210829-46-2P 210830-02-7P 210830-13-0P 210830-31-2P 210830-35-6P 210830-59-4P (preparation of exendin peptides for the reduction of food intake) L31 ANSWER 9 OF 11 USPATFULL on STN 2002:92629 USPATFULL ΑN Long lasting insulinoptropic peptides TIBridon, Dominique P., Outremont, CANADA TN L'Archeveque, Benoit, Leval, CANADA Ezrin, Alan M., Moraga, CA, UNITED STATES Holmes, Darren L., Montreal, CANADA Leblanc, Anouk, Montreal, CANADA St. Pierre, Serge, Ile Bizard, CANADA US 2002049153 20020425 Α1 PΙ US 6593295 В2 20030715 20010606 (9) US 2001-876388 Α1 ΑI

RLI Division of Ser. No. US 2000-623618, filed on 5 Sep 2000, PENDING A 371 of International Ser. No. WO 2000-US13563, filed on 17 May 2000, UNKNOWN

PRAI US 1999-159783P 19991015 (60) US 1999-134406P 19990517 (60)

DT Utility FS APPLICATION

LREP Michael R. Ward, Morrison & Foerster LLP, 425 Market Street, San Francisco, CA, 94105-2482

CLMN Number of Claims: 19 ECL Exemplary Claim: 1

DRWN No Drawings

LN.CNT 2355

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Modified insulinotropic peptides are disclosed. The modified insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5

(lasting insulinotropic pepwith antidiabetic activity)

IT 308245-55-8 308806-01-1 308815-99-8

309729-80-4

(long lasting insulinotropic peptides with antidiabetic activity)

```
308244-92-0P 308249-19-6P 309728-25-4P
ΙT
      309729-78-0P 309729-82-6P
        (long lasting insulinotropic peptides with antidiabetic activity)
L31 ANSWER 10 OF 11 USPATFULL on STN
       2001:226593 USPATFULL
ΑN
       Long lasting insulinotropic peptides
ΤI
       Bridon, Dominique P., Outremont, Canada
IN
       L'Archeveque, Benoit, Laval, Canada
       Ezrin, Alan M., Moraga, CA, United States
       Holmes, Darren L., Montreal, Canada
       Leblanc, Anouk, Montreal, Canada
       St. Pierre, Serge, Ile Bizard, Canada
       Conjuchem, Inc., Montreal, Canada (non-U.S. corporation)
PΑ
                          B1 20011211
PΙ
       US 6329336
       WO 2000069911 20001123
                               20000905 (9)
       US 2000-623618
ΑI
       WO 2000-US13563
                               20000517
                               20000905 PCT 371 date
                               20000905 PCT 102(e) date
                           19990517 (60)
PRAI
       US 1999-134406P
       US 1999-159783P
                           19991015 (60)
DT
       Utility
       GRANTED
FS
      Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Strzelecka,
EXNAM
       Teresa
       Morrison & Foerster LLP
LREP
       Number of Claims: 14
CLMN
       Exemplary Claim: 1
ECL
DRWN
       No Drawings
LN.CNT 2101
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
       Modified insulinotropic peptides are disclosed. The modified
       insulinotropic peptides are capable of forming a peptidase stabilized
       insulinotropic peptide. The modified insulinotropic peptides are capable
       of forming covalent bonds with one or more blood components to form a
       conjugate. The conjugates may be formed in vivo or ex vivo. The modified
       peptides are administered to treat humans with diabetes and other
       related diseases.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
        (lasting insulinotropic pepwith antidiabetic activity)
     308245-55-8 308806-01-1 308815-99-8
IT
      309729-80-4
        (long lasting insulinotropic peptides with antidiabetic activity)
     308244-92-0P 308249-19-6P 309728-25-4P
IT
      309729-78-0P 309729-82-6P
        (long lasting insulinotropic peptides with antidiabetic activity)
L31 ANSWER 11 OF 11 USPAT2 on STN
       2002:92629 USPAT2
ΑN
       Long lasting insulinotropic peptides
TI
       Bridon, Dominique P., Outremont, CANADA
ΙN
       L'Archeveque, Benoit, Laval, CANADA
       Ezrin, Alan M., Moraga, CA, United States
       Holmes, Darren L., Montreal, CANADA
       Leblanc, Anouk, Montreal, CANADA
       St. Pierre, Serge, Ile Bizard, CANADA
       Conjuchem, Inc., Montreal, CANADA (non-U.S. corporation)
PΑ
       US 6593295
                          B2
                               20030715
PΙ
       US 2001-876388
                                20010606 (9)
ΑI
       Division of Ser. No. US 623618, now patented, Pat. No. US 6329336
RLI
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PRAI US 1999-134406P 19990517 (60) US 1999-159783P 19991015 (60)

DT Utility FS GRANTED

EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Strzelecka,

LREP Morrison & Foerster LLP CLMN Number of Claims: 29

ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)

LN.CNT 2354

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Modified insulinotropic peptides are disclosed. The modified insulinotropic peptides are capable of forming a peptidase stabilized insulinotropic peptide. The modified insulinotropic peptides are capable of forming covalent bonds with one or more blood components to form a conjugate. The conjugates may be formed in vivo or ex vivo. The modified peptides are administered to treat humans with diabetes and other related diseases.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

IT 309729-73-5

(lasting insulinotropic pepwith antidiabetic activity)

IT 308245-55-8 308806-01-1 308815-99-8 309729-80-4

(long lasting insulinotropic peptides with antidiabetic activity)

IT 308244-92-0P 308249-19-6P 309728-25-4P

309729-78-0P 309729-82-6P

(long lasting insulinotropic peptides with antidiabetic activity)

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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 50 summaries
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Maximum DB seq length: 200000000
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published Applications AA:*

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2: /cgn2 6/ptodata/1/pubpaa/IS06 NEW PUB.pep:*

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121
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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, 444.	۲ ۲	Appl	4, App	o, App	ישלי	י לילי לילי	ייייייייייייייייייייייייייייייייייייי	App), App	App1	Appl	1, App	J. ADD	1	777	21:00	מילים ל	יייי ל לייייי ליייייייייייייייייייייייי										יייי בייייי דייייייייייייייייייייייייייי	יייי ביייי דיייייייייייייייייייייייייייי	ייי ליין קייין ליין קייין ליין	Appl	ייים מיים מיים	App.	Appl	Appl	Appl	Appl

ALIGNMENTS

RESULT 1

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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF TITLE OF INVENTION: USE OF EXENDINS AND TREATMENT OF DYSLIPIDEMIA FILE REFERENCE: 249/124
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION UNDER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PATENTIN ONS: 188
SOFTWARE: PATENTIN Ver 2.1
CRGAMTT:
                                                                                         APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: O9/889,330
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
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US-10-157-224A-171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                          SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 171
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
ORGANISM: Artificial Sequence
                                        ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%; Score 93; DB 11
Similarity 65.6%; Pred. No. 2e-09;
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PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR PRIOR DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
NUMBER OF EXE ID NOS: 188
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 171
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                                                                                                       US-09-003-869-99
Sequence 99, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
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Publication No. US20030087821A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
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APPLICANT: PRICKETT,
APPLICANT: BHAVSAR, S
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: artificially synthesized sequence of novel exendin OTHER INFORMATION: agonist
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65.6%; Pred. No. 2e-09;
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65.6%;
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CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08

EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER: OF SEQ ID NOS: 188
SOFTWARE: FASTESQ for Windows Version 3.0
SEQ ID NO 99
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE: THEORYTICAL Artificially Synthesized
                                                                                                                                                                                                                                                                                                               APPLICANT: BESLEY, NIGEL ROBERT ARNOLD
APPLICANT: BRACKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
ITILE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
ITITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/161
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-01-07
EARLIER REPLICATION NUMBER: US 60/065,442
EARLIER REPLICATION NUMBER: US 60/065,442
EARLIER REPLICATION NUMBER: US 60/065,029
EARLIER REPLICATION NUMBER: US 60/066,029
EARLIER REPLICATION DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTMARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 183
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Patent No. US20020137666A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (37)...(37)
OTHER INFORMATION: amidated hPro (homoprolinamide)
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NAME/KEY: AMIDATION LOCATION: (37)...(37) OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
                                                                                                                                                         OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
                                                                                                                                                                                                                                    LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     FEATURE:
                                                                                                          OTHER INFORMATION: Xaa
                                                                                                                                       FEATURE:
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Similarity 68.8%;
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                                                                                                             positions
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Pred. No.
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                                                                                                                31,
                                                                                                                36 and
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                                                                                                                   37 stands
                                                                                                                   for n-methylalanine
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           Sequence 183, Application US/09756690A

Publication No. US20030036504A1

Publication No. US20030036504A1

GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.

APPLICANT: YOUNG, ANDREW A.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA FILE REFERENCE: 249/124

FILE REFERENCE: 249/124

CURRENT APPLICATION NUMBER: US/09/756,690A

CURRENT FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/175,365

PRIOR FILING DATE: 2000-01-10
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APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REPERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ. ID NOS: 188
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NUMBER OF SEQ ID NOS: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: (37)
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: hPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: c-term amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (36)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93; DB 11; Length 37; Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR TILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER: 05 SEQ ID NOS: 188
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                                    NAME/KEY: MOD RES
LOCATION: (36)..(37)
OTHER INFORMATION: Homoproline
US-10-157-224A-99
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SEQ ID NO 183
LENGTH: 37
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SEQ ID NO 99
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
FILE REFERENCE: 02001-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MOD RES
(31)
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OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
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LOCATION: (37)
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OTHER INFORMATION: NMeala
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LOCATION: (36)
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                                                                                                                                                                 NAME/KEY: MOD_RES
LOCATION: (31)
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                                                                                                                                                                                                                                                                                               FEATURE:
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    76.9%;
      Score 93;
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         DB 15;
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      Length 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: N-methylalanine US-10-157-224A-183
                                                                                                                                                                                                                                                                                               RESULT 11
US-10-187-051-99
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Publication No. US20030087820A1
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                                                                                             Sequence 99, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: BHAYSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
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TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADVEL EXENDIN THEREOF
FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
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Best Local Similarity
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PRIOR FILING DATE: 2001-07-13
PRIOR PELICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
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PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
                    CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
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LOCATION: (36)..(
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LOCATION: (31)
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0; Mismatches 10;
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Pred. No. 2.1e-09;
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PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PastSEQ for Windows Version 3.0
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SEQ ID NO 183
LENGTH: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR PELICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
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NUMBER OF SEQ ID NOS: 188
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: artificia OTHER INFORMATION: agonist OTHER INFORMATION: compound
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                                                                                                                                        FEATURE: OTHER INFORMATION: artificially synthesized sequence of novel exendin OTHER INFORMATION: agonist
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                                                                   OTHER INFORMATION: Xaa in positions 31, OTHER INFORMATION: methylalanine.
                                                                                                                                      OTHER INFORMATION: agonist OTHER INFORMATION: compound
                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                          FEATURE:
                                                                                                               FEATURE:
LOCATION: (37)...(37)
                   NAME/KEY: AMIDATION
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
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APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
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                                                                                                                                                                                    Sequence 36, Application US/09003869A Patent No. US20020137666A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                              APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
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22; Conservative
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pred. No. 2.1e-09;
0; Mismatches 10
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Pred. No. 2.2e-09;
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EARLIER FILING DATE: 1997-01-07

EARLIER APPLICATION NUMBER: US 60/055,404

EARLIER FILING DATE: 1997-08-08

EARLIER APPLICATION NUMBER: US 60/065,442

EARLIER FILING DATE: 1997-11-14

EARLIER APPLICATION NUMBER: US 60/066,029

EARLIER FILING DATE: 1997-11-14

NUMBER OF SEQ ID NOS: 188

SOPTWARE: FASESEQ for Windows Version 3.0

SEQ ID NO 36

LENOTH: 39

TYPE: PRI
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US-09-003-869-39
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                                                              NAME/KEY: AMIDATION
LOCATION: (39)...(39)
COTHER INFORMATION: amidated Ser (Serinamide)
US-09-003-869-39
                                                                                                                                                                                                                                                                                                                                                                                                           PILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,404
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
EARLIER FILING DATE: 1997-11-14
NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER: US 60/066,029
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Patent No. US200
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LENGTH: 39
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APPLICANT: RRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
Query Match
Best Local Similarity
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OTHER INFORMATION: amidated Ser (Serinamide)
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                                                                                                                                                                                                                            OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
                                                                                                                                                                               OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for n-methylalanine
                                                                                                                                                                                                                                                                              FEATURE:
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Pred. No. 2.2e-09;
0; Mismatches 10
     Score 93;
Pred. No.
       DB 10; Length 39; 2.2e-09;
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CURRENT FILING DATE: 2002-04-19
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver 2.1
SEQ ID NO 35
LENGTH: 39
                                                                                                                                                                                                                                                         US-09-756-690A-36
              APPLICANT: YOUNG, ANDREW A.

APPLICANT: YOUNG, ANDREW A.

APPLICANT: YOUNG, ANDREW A.

TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR MODULATION OF TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA FILE REFERENCE: 249/124

FILE REFERENCE: 249/124

CURRENT APPLICATION NUMBER: US/09/756,690A

CURRENT FILING DATE: 2000-04-19

PRIOR APPLICATION NUMBER: 60/175,365

PRIOR APPLICATION NUMBER: 60/175,365

PRIOR FILING DATE: 2000-01-10
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APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USB OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
                                                                                                                                                                                                             Sequence 36, Application US/09756690A Publication No. US20030036504A1
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ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 188
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OTHER INFORMATION:
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Similarity 68.8%;
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Pred. No. 2
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SOFTWARE: PatentIn Ver 2.1 SEQ ID NO 36
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                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/175,365
PRIOR ETLING DATE: 2000-01-10
PRIOR ETLING DATE: 2000-01-10
NUMBER OF SEO ID NOS: 188
SOFTWARE: Patentin Ver 2.1
SEQ ID NO 39
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
US-09-756-690A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: tPro
                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/09756690A publication No. US20030036504A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: tPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (38)
OTHER INFORMATION: tPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: tPro
                                                                                                                                                                                                                                                                                  APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: c-term amidation
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/756,690A CURRENT FILING DATE: 2002-04-19
                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                           ORGANISM: Artificial Sequence
                                                        OTHER INFORMATION: MeAla
                                REATURE: MOD_RES
                                                                        NAME/KEY: MOD RES
OTHER INFORMATION: MeAla
                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GTXXXXXXKQXEEEAVRLXXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.9%; Score 93; DB 11; nilarity 68.8%; Pred. No. 2.2e-09; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 39;
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NAME/KEY: MOD_RES

US-10-157-224A-36

; Sequence 36, Application US/10157224A publication No. US20030087820A1

GENERAL INFORMATION

APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
TITLE OF INVENTION: ADMINISTRATION THEREOF

INFORMATION: MeAla

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APPLICANT: YOUNG, ANDRON A:
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
TITLE OF INVENTION: ADMINISTRATION THEREOF
TITLE OF INVENTION: ADMINISTRATION THEREOF
TILLE REFERENCE: 02001-05-28
CURRENT FILING DATE: 2002-05-28
CURRENT FILING DATE: 2002-07-13
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR APPLICATION NUMBER: FCT/US00/00902
PRIOR APPLICATION NUMBER: FCT/US00/00902
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 50/175,365
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US-10-157-224A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: c-term amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MeAla
                                                                                                                                                                                                                                                        US-10-157-224A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 35
8
                                                                                                                          Matches
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (36)...(38)
OTHER INFORMATION: thioproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (31)
OTHER INFORMATION: thioproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 68.8
22; Conservative
                                                                                                                                                      , Match 76.9%; Score 93; DB 15; Length 39; Local Similarity 68.8%; Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GTFTSDLSKQLÉEÉAVRLFIEFLKNGGXSSGA 35
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                                                                  4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
   4 GTFTSDLSKQLEEEAVRLFTEFLKNGGXSSGA 35
                                                                                                                                        Conservative
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CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-14
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1990-01-14
PRIOR FILING DATE: 1990-01-10
PRIOR FILING DATE: 2000-01-10
PRIOR PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR FILING DATE: 2000-01-10
PRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILLE OF INVENTION OF SEQ ID NOS 188

PILE REFERENCE: 02001-050

PRICE APPLICATION NUMBER: US/10/157,224A

CURRENT FILING DATE: 2002-05-28

PRICE APPLICATION NUMBER: 09/889,330

PRICE FILING DATE: 2000-01-14

PRICE FILING DATE: 2000-01-14

PRICE FILING DATE: 2000-01-14

PRICE FILING DATE: 1999-01-14(380)

PRICE APPLICATION NUMBER: 60/175,365

PRICE APPLICATION NUMBER: 60/175,365

PRICE FILING DATE: 1999-01-14

PRICE FILING DATE: 1999-01-14

PRICE APPLICATION NUMBER: 60/175,365

PRICE FILING DATE: 2000-01-10

PRICE FILING DATE: 1999-01-14

PRICE FILING 
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OTHER INFORMATION: homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KOLTERWAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 39
                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                OTHER INFORMATION: c-term amidation
                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                     ENGTH:
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                                                                                                                                                                                                                                                                   RESULT 23
                                      Sequence 36, Application US/10187051
publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
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FEATURE:

NAME/KEY: MOD RES

LOCATION: (36)..(38)

OTHER INFORMATION: N-methylalanine
US-10-157-224A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
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US-10-187-051-35
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                                                                                                                                                         NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BEELEY,
APPLICANT: PRICKE'
APPLICANT: BHAVSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
                                                                                                   Query Match
Best Local Similarity
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 76.9%;
Local Similarity 68.8%;
Local Similarity 68.8%;
es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: artificially synthesized sequence of novel exendin
                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for OTHER INFORMATION: thioproline.
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
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                                                                            22; Conservative
                                    US20030087821A1
GTFTSDLSKOLÉEÉÁVRÍFIEFÍKNGGXSSGÁ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIGEL ROBERT ARNOLD
                                                                                                                                                                                                                                                                                                                                           compound
                                                                                                                                                                                                                                                                                                                                                             agonist
                                                                                                         76.9%; Score 93; DB 15; 68.8%; Pred. No. 2.2e-09;
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pred. No. 2.2e-09;
                                                                                                0; Mismatches
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                                                                                                                                           DB 15; Length 39;
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FILLE OF INVENITION TO THE PRICE PRICE 231/181

FILE REFERENCE: 231/181

CURRENT APPLICATION NUMBER: US/10/187,051

CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/09/003,869

PRIOR APPLICATION NUMBER: US 60/034,905

PRIOR APPLICATION NUMBER: US 60/055,404

PRIOR PILING DATE: 1997-01-07

PRIOR APPLICATION NUMBER: US 60/065,442

PRIOR APPLICATION NUMBER: US 60/065,442

PRIOR APPLICATION NUMBER: US 60/065,442

PRIOR APPLICATION NUMBER: US 60/066,029

PRIOR PILING DATE: 1997-11-14

PRIOR FILING DATE: 1997-11-14
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   APPLICANT: BELLETT, KATHRYN S.
APPLICANT: BHAUSAR, SUMIL
TITLE OF INVENTION: USE OF EXEMDINS AND AGONISTS THEREOF FOR TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
TITLE OF INVENTION: USE OF SOOD OF SOOTWARE: FASTSOO FOR MINDER: US 60/066,029
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
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Sequence 39, Application US/10187051

Sequence NO. US20030087821A1

Publication NO. US20030087821A1
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GENERAL INFORMATION:

APPLICANT: BELEY, NIGEL ROBERT ARNOLD

APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: BHAVSAR, SUNIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: amidated Ser (Serinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: AMIDATION LOCATION: (39)...(35
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22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĠTFTSDLŚKÓLĖĖĖAVRLFIEFLKNGGXŚŚGA 35
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; Sequence 173, Application US/09003869A
; Patent No. US20020137666A1
. GENERAT. INFORMATION:
                                                                                           US-09-003-869-173
                                                                                                                                  RESULT 26
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APPLICANT: BEELEY, NIGEL ROBERT ARNOLD APPLICANT: BEELEY, NIGEL ROBERT ARNOLD APPLICANT: BHAVSAR, SUNIL APPLICANT: BHAVSAR, SUNIL APPLICANT: BHAVSAR, SUNIL TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THE TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE TITLE OF INVENTION UNMBER: US/09/003,869A CURRENT APPLICATION NUMBER: US/09/003,869A CURRENT FILING DATE: 1998-01-07 CURRENT FILING DATE: 1997-01-07 EARLIER APPLICATION NUMBER: US/09/034,905 EARLIER FILING DATE: 1997-08-08 EARLIER FILING DATE: 1997-08-08 EARLIER FILING DATE: 1997-11-14 EARLIER APPLICATION NUMBER: US/09/065,442 EARLIER FILING DATE: 1997-11-14 SARLIER FILING DATE
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                                                                                                                                                                                     Query Match
                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                          FEATURE: FAIDATION NAME/KEY: AMIDATION LOCATION: (35)...(35) OTHER INFORMATION: amidated Ala (Alaninamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Similarity 68.8%;
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                                                                                                            76.0%; Score 92; DB 10;
1 Similarity 65.6%; Pred. No. 2.9e-09;
21; Conservative 0; Migmarchical
                                                              4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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4 GTFTSDLSKÓLEBEAVRLFIEFLKNGGPSSGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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pred. No. 2.2e-09;
                                                                                                                                                     0; Mismatches 11;
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CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-11-14
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-756-690A-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 69, Application US/09756690A
publication No. US20030036504A1
                                                                                                                                                                US-09-756-690A-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: AMIDATION
LOCATION: (35)...(35)
OTHER INFORMATION: amidated Ala (Alaninamide)
                                                                                                                                                                                                                                                                                                                                                   PILE REPERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
CURRENT FILING DATE: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
SEC ID NOS: 188
SOFTMARE: Patentin Ver 2.1
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOLTERMAN, ORVILLE G. APPLICANT: YOUNG, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                  Query Match
Best Local :
                                                                                Matches
                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                         FEATURE
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                                                                                                                                                                                     INFORMATION: c-term amidation
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Similarity 65.6%;
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                                      4 GTXXXXXXKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                         Similarity
GTFTSDLSKQLEEBAVRLFIBFLKNGGPSSGA 35
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                                                                                       Conservative
                                                                                                           76.0%; Score 92; DB 11; Length 35; 65.6%; Pred. No. 2.9e-09;
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pred. No. 2.9e-09;
0; Mismatches 1:
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RESULT 28
US-09-756-690A-173
US-09-756-690A-173, Application US/09756690A
Sequence 173, Application US20030036504A1
Publication No. US20030036504A1
Publication No. US20030036504A1
PUBLICATION ORVILLE G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: c-term amidation US-09-756-690A-173
                                                                                                                                                                                                                                                                          CURRENT FILING DATE: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 69
LENGTH: 35
TYDER: DATE: 35
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APPLICANT: YOUNG, ANDREW A.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
TITLE OF INVENTION NUMBER: US/09/756,690A
CURRENT APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR PILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-01-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/10157224A publication No. US20030087820A1 publication No. US20030087820A1 GENERAL INFORMATION: APPLICANT: YOUNG, ANDREW A. APPLICANT: KOLTERMAN, ORVILLE G. APPLICANT: KOLTERMAN, ORVILLE G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 173
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                                                                                                                            ; FEATURE:
; OTHER INFORMATION: c-term amidation
US-10-157-224A-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist FEATURE:
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                                      Best Local Similarity
Matches 21; Conserv
                                                                                 Query Match
                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GTXXXXXSKQXESEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTFTSDLSKOLEEEAVRLFIEFLKNGGPSSGA 35
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4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 92; DB 11;
65.6%; Pred. No. 2.9e-09
                                                                            76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                 Score 92; DB 15;
Pred. No. 2.9e-09;
                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 35
                                                                                                              DB 15;
                                                                                                                   Length 35;
                                                                                 0
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                                                                                      Gaps
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Page 11

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US-10-157-224A-173
US-10-157-224A-173
Sequence 173, Application US/10157224A
Sequence 173, Application US/20030087820A1
Publication No. US20030087820A1
Publication No. US20030087820A1
Publication No. US20030087820A1
PUBLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT ON NOW ADMINISTRATION THEREOF
FILTE OF INVENTION: ADMINISTRATION THEREOF
FILTE REFERENCE: 02001-050
FILE REFERENCE: 02001-050
FILE REFERENCE: 02001-05-28
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR APPLICATION NUMBER: 09/105/00902
PRIOR APPLICATION NUMBER: 00/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR PILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 173
LENGTH: 35
TYPE- NRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             망
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist; FEATURE: OTHER INFORMATION: c-term amidation US-10-157-224A-173
Search completed: December 23, 2003, 10:12:01 Job time : 25.5 secs
                                                                                                                                                                   8
                                                                                                                      밁
                                                                                                                                                                                                                                Query Match 76.0%; Score 92; DB 15; Length 35; Best Local Similarity 65.6%; Pred. No. 2.9e-09; Matches 21; Conservative 0; Mismatches 11; Indels Matches 21; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTXXXXXŞKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                      4 GTFTSDLSKQLEEEAVRLFIEFLKNGGPSSGA 35
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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Maximum DB
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Maximum Match 100%
Listing first 50 summaries
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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173.947 Million cell updates/sec
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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11:
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199.DAT:
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3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199.DAT:
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9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query Query Query DB ID

NO. Score Match Length DB ID

AAY17618 Exendin agonist pe 94 77.7 37 22 AAE08527 Exendin agonist pe 94 77.7 37 22 AAE08527 Exendin agonist pe 95 76.9 36 20 AAY17606 Exendin agonist pe 96 93 76.9 36 21 AAB53029 Amino acid sequence 97 93 76.9 36 21 AAR94184 Amino acid sequence 97 93 76.9 36 21 AAR94184
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5444443	4 4 D D D D D D D D D D D D D D D D D D	0 1
	93 76.9 93 76.9	76
	377 220 377 22	
2 AAB64249 2 AAB64353 2 AAP64353 2 AAY31533 0 AAY24856 0 AAY24837 0 AAY17619 0 AAY17619 1 AAB111159	NAY2485 NAY2485 NAY2485 NAY248127 NAR5304 NAR5884 NAR5884 NAR5884 NAR588 NAR588 NAR588 NAR588 NAR588 NAR588 NAR588 NAR588 NAR588 NAR588	AE085
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agonist, S agonist pe agonist pe agonist pe agonist pe agonist pe agonist pe agonist pe	set ender see to be see to	44,44

ALIGNMENTS

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RESULT 1
AAY17618
AAY17618 standard; peptide; 37 AA.
                                                                                                                         Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                              Exendin agonist peptide #84.
                                                                                                                                                                                 09-AUG-1999
                                                                                                                                                                                                   AAY17618;
                                                                                                           Synthetic.
                                                                                WO9925728-A1.
                           14-NOV-1997;
                                             13-NOV-1998;
                                                               27-MAY-1999
                                                                                                 Heloderma sp
         (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                   (first entry)
                             97US-0066029
                                              98WO-US24273.
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RESULT 2
AAE08527
ID AAE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are peptides that are found in the venom of the Gila-monster, a lizard peptides to Arizona and Northern Mexico. The peptide agonists are endogenous to Arizona and Northern Mexico. The peptide agonists are used to treat diabetes mellitus (types I or II), hyperglycaemia or hypoglycaemia. They can also be used for in vitro and in vivo studies on exendins and their agonists. They regulate gastric motility and slow gastric emptying (resulting in lower post-prandial glucose levels).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide agonists of exendin - delay stomach emptying, for treating diabetes and hypo- or hyper-glycaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 28; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-347456/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin agonist peptide #172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE08527 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                       10-JAN-2000; 2000US-0175365
                                                                                                                                                                                                                         19-JUL-2001
                                                                                                                                                                                                                                               WO200151078-A1
                                                            triglyceride levels, and treating heart disease
                                                                                                                                                                                                09-JAN-2001; 2001WO-US00719
                                     Example 178; Page 143; 161pp; English.
                                                                                                WPI; 2001-514422/56.
                                                                                                                        Kolterman OG,
                                                                                                                                                  (AMYL-) AMYLIN PHARM INC
                                                                       of exendin and exendin agonist compounds for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTFTSALSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prickett KS;
                                                                                                                            Young AA
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                        /note= "N-methyl alanine; C-terminal amide"
                                                                                                                                                                                                                                                                                                                          /note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                               /note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37;
                                                                         dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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AAB64363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB64363 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin agonist, SEQ ID NO:183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB64363;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                       Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                         WO200073331-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a sub-
                                                                                                                                                                                                                                                                                   Hiles R, Prickett KS;
                                                                                                                                                                                                                                                                                                                             01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                               23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                     07-DEC-2000
                                                                                                                                                                                                                         especially in a human
                                                                                                                                                                                                                                                                  WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                        (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTFTSALSKOMEEEAVRLFIEWLKNGGASSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                               99US-0323867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 94; DB 22;
Pred. No. 5.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                               subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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The invention relates to the use of an exendin (AAB64181-B64182) or CC an exendin agonist (AAB64185-B64368) for treating gestational diabetes cc mellitus (GDM) in a patient GDM arises during pregnancy, and is due controlled to the combination of increased insulin resistance and a diminished cc to a combination of increased insulin resistance and an exerction increase. GDM cc pregnancy, both insulin resistance and insulin secretion increase. GDM cc pregnancies are associated with complications in both the mother and the cc pregnancies are associated with complications in both the mother and the cc pregnancies are associated with complications in both the mother and the cc infections. GDM results in an elevated rate of Caesarian delivery. CC hypertensive disorders such as pre-eclampsia, and urinary tract cc infections. GDM results in an elevated rate of foetal abnormalities such cc neonatal morbidites such as hypoglycaenia, hypocalcaemia, of complete controlled for the secretions of the Gila monster (exendin-4) and the Mexican beaded lizard cc secretions of the Gila monster (exendin-4) and the Mexican beaded lizard (cc sundin-1) which exhibit homology with several members of the cc secretions of the Sila monster (exendin-4) and the Mexican beaded lizard cc secretions of the Sila monster (exendin-1) and have similar cc diabetes, which are contraindicated for GDM, exendins and exendin Example 178; Page 119; 133pp; English.

The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an triglyceride and other lipid levels by administering exendin or an triglyceride and other lipid levels by administering exending have inotropic and diuretic effects. They

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                     Matches
                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agonists do not cross the placenta and thus do not cause severe prolonged hypoglycaemia in the newborn. They have a potent and prolonged effect on blood glucose, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The present sequence represents a exendin agonist of the invention which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   based upon the sequence of exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exendin agonist peptide SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma glucose; gastric emptying; food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB11313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB11313 standard; Peptide;
                                                                                                                                            This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200041546-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000
                                                                                                                                                                                                                                                                                                 New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat
                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-1999;
                                                                                                                                                                                                                                                         Example 44; Figure 15; 281pp; English.
                                                                                                                                                                                                                                                                                                                                            WPI; 2000-514584/46.
                                                                                                                                                                                                                                                                                                                                                                                                    (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2000; 2000US-0116380
                                                                                                          Sequence
                                                                                                                                   or reducing food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTFTSALSKOMEEBAVRLFIEWLKNGGASSGA 35
                                                                     Similarity
                         GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                         L'Italien JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 AA;
GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                             39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                9908-0116380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.7%;
                                                                     77.7%;
                                                                                                                                                                                                                                                                                                                                                                              Kolterman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB 22;
Pred. No. 5.2e-10;
0; Mismatches 11
                                                         0
                                                                     Score 94; DB 21;
Pred. No. 5.5e-10;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 37;
                                                                         Se-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                     Length 39;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                               0
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RESULT

AAY17606;

AAY17606 standard; peptide; 36 AA

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RESULT 5
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 밁
                       S
                                                      Matches
                                                                   Best
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE08383 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exendin agonist peptide #30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE08383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                  The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride a significant effect on the reduction of blood serum triglyceride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2001; 2001WO-US00719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200151078-A1
                                                                                                                               concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin. Note: The present sequence is not shown in the specification but is derived from SEQ ID NO:3 shown in page 17 of the specification.
                                                                                                                                                                                                                                                                                                                Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                                     Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JAN-2000; 2000US-0175365
                                                                                                                                                                                                                                                                                    Example 30; Page -; 161pp; English.
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               (AMYL-) AMYLIN PHARM INC
                                                                 Local
4 GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA
                          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                             39 AA;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-Methyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-Methyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-Methyl-alanine"
                                                                    77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-Methyl-alanine"
                                                          0
                                                                      Score 94; DB 22;
Pred. No. 5.5e-10;
                                                          Mismatches
        35
                                                                                       Length 39;
                                                              Indels
                                                                0
                                                                 Gaps
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RESULT 7
AAB11263
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Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exendin agonist peptide #72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                            AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are peptides that are found in the venom of the Gila-monster, a lizard peptides to Arizona and Northern Mexico. The peptide agonists are endogenous to Arizona and soliting for II), hyperglycaemia or used to treat diabetes mellitus (types I or II), hyperglycaemia or hypoglycaemia. They can also be used for in vitro and in vito studies on exendins and their agonists. They regulate gastric motility and slow gastric emptying (resulting in lower post-prandial glucose levels).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09925728-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heloderma sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 28; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes and hypo- or hyper-glycaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide agonists of exendin - delay stomach emptying, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-347456/29
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                         Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
                                                                                                                                                exendin agonist peptide SEQ ID NO 171.
                                                                                                                                                                                                                     AAB11263 standard; Peptide; 36
                                                                                           Synthetic
                                                                                                                plasma glucose;
                                                                                                                                                                         20-FEB-2001
                                                                                                                                                                                                 AAB11263;
                                             20-JUL-2000
                                                                 WO200041546-A2
                     10-JAN-2000; 2000US-0116380.
                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                               4 GTFTSDASKOLEEBAVRLFIEFLKNGGPSSGA 35
                                                                                                                                                                                                                                                                                                      4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prickett KS;
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0066029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US24273.
                                                                                                                gastric emptying; food intake.
                                                                                                                                                                                                                                                                                                                                            76.9%;
                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                            Score 93; DB 20; Length 36; Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             문
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             AAB53029;
                                                                                                                                                                                                                                                                                                                     Heloderma sp.
The present invention relates to extendins and their agonists which have been modified with molecular weight increasing agents such as polyethylene glycol (PEG). These can be used in the treatment of diabetes, obesity, impaired glucose tolerance, postprandial dumping syndrome, postprandial hyperglycaemia, eating disorders, insulin resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
                                                                                                                                                                                                                                                                        09-NOV-2000
                                                                           Disclosure; Fig 4; 119pp; English.
                                                                                                                                                                                                                         30-APR-1999;
                                                                                                                                                                           Young A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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14-JAN-1999;

99US-0116380.

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This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-514584/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 180; Page 229; 281pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or reducing food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Extendin agonist compound #157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB53029 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                              dyslipidaemia; insulin-resistance syndrome;
                                                                                                                                                                                                                                                                                                                                                                                              Extendin; agonist; diabetes; obesity; eating disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2001 (first entry)
Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity -
                                                                                                                                                                                                                                                                                                        WO200066629-A1
                                                                              WPI; 2000-672834/65.
                                                                                                                                                       (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                             28-APR-2000; 2000WO-US11814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTFTSDASKOLEBEAVRLFIEFLKNÖGPSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L'Italien JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 AA;
                                                                                                                      Prickett K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                               99US-0132018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolterman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DB 21;
Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY94184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                      The present sequence represents a modified extendin or extendin agonist. Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic crythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of an extendin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY94184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY94184 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-1999; 99US-0116380.
30-APR-1999; 99US-0132017.
10-JAN-2000; 2000US-0175365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heloderma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                        Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2000; 2000WO-US00942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200041548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                         Disclosure; Fig 4G; 96pp; English.
                                                                                                                                                                                                                                                                                                                      WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                                                                                                  (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTFTSDASKOLEEBAVRLFIEFLKNGGPSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                       Gedulin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%; Score 93; DB 21; Length 36; 65.6%; Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Query Match

1

76.9%; Score 93; DB 21; Length 36; 6%. Pred. No. 7.7e-10;

RESULT 11 AAB64351

AAB64351 standard; peptide; 36 AA

0

X I X R

27-MAR-2001 AAB64351;

(first entry)

Sequence

36 AA;

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AAE08515
ID AAE(
XX
AC AAE(
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
밁
                                                      Matches
                                                                  Best Local
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendin agonist peptide #160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE08515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE08515 standard; peptide;
                                                                                                                                 The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200151078-A1.
                                                                                                                                                                                                                                                                                         Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                  Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-2001; 2001WO-US00719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                               Example 166; Page 136; 161pp; English.
                                                                                                                                                                                                                                                                                                                                      WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2000; 2000US-0175365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2001
                                                                                                         Sequence
                                                    21; Conservative
                         4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĠŤFTSDASKOLĖĖĖAVRLFIEFLKNGGPŚSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                h 76.9%; Score 93; DB 22; Similarity 65.6%; Pred. No. 7.7e-10;
GTFTSDASKOLEEEAVRLFIEFLKNGGPSSGA 35
                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
6
                                                         0
                                                         Mismatches
                                                                                    DB 22; Length 36;
                                                             0
                                                               Gaps
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constitution of insulin secretion. In contrast, in a normal science and insulin secretion increase. GDM CC pregnancy, both insulin resistance and insulin secretion increase. GDM CC pregnancies are associated with complications in both the mother and the CC pregnancies are associated with complications in both the mother and the CC pregnancies are associated with complications in both the mother and the CC pregnancies. Women with GDM have increased rates of Caesarian delivery, CC pregnancies which as pre-eclampsia, and urinary tract confections. GDM results in an elevated rate of foetal abnormalities such as increased risk of CC as neural tube defects, and is associated with an increased risk of CC neonatal morbidites such as hypoglycaemia, hypocalcaemia, and subsequent CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent CC childhood and adolescent obesity. Exendins are peptides from the salivary CC (exendin-3) which exhibit homology with several members of the CC (exendin-3) which exhibit homology with several members of the CC (exendin-3) which exhibit homology with several members of the CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effects. Unlike the compounds used to treat type 2 CC insulinotropic effec
                                                                                                                                  RESULT 12
AAY24869
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BXXXXX
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pregnancy complication; neonatal abnungulinotropic; anorectic; exendin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin agoniat; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiles R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabetes mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 166; Page 113; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      especially in a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                AAY24869 standard; peptide; 37 AA
                 24-AUG-1999
                                                                       AAY24869;
                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prickett KS;
                                                                                                                                                                                                                                    ĠŢFTSDAŚKQLĖĖĖAVRLFIEFLKNGGPŠŚĠA 35
                                                                                                                                                                                                                                                                                     GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                    36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the sequence of exendin-4.
                                                                                                                                                                                                                                                                                                                                     Conservative
                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0323867.
                                                                                                                                                                                                                                                                                                                                                            76.9%;
                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 22;
Pred. No. 7.7e-10;
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 36;
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TY SON THE STATE OF THE STATE O

27-MAY-1999

Synthetic. Heloderma sp W09925727-A2 Exendin agonist peptide #45.

24-AUG-1999

(first entry)

AAY24853 standard; peptide; 37

Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.

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Matches
                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin agonist peptide #61.
                                                                                                                                                                                                                                                                                    regulate gastric motility and slow gastric emptying. The peptides can be used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic conditions. The peptides are exendin agonists which have activity as agents to regulate gastric motility and to slow gastric emptying, as agents to ability to reduce post-prandial glucose levels in evidenced by the ability to reduce post-prandial glucose levels in mammals. They can be used for the treatment of Type I and II diabetes and hyperglycaemic or hypoglycaemic conditions. They can also be used for the treatment of disorders which would be benefited by agents which lower plasma glucose levels and in treatment of disorders which would be benefited with agents useful in delaying and/or slowing gastric emptyrica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09925727-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New exendin agonist peptides - can regulate gastric motility and slow gastric emptying, used for treating, e.g. diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-394773/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY24809 to AAY24877 represent exendin agonist peptides which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Fig 4; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                     emptying.
                                                                                                                               Local Similarity
                                                                                                        22; Conservative
                                                    4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
GTFTSDASKOMEEBAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                       37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prickett KS;
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                                                                                                                                        76.98;
                                                                                                                    0
                                                                                                                                        Score 93;
Pred. No.
                                                                                                                       Mismatches
                                                                                                                                                 8e-10;
                                                                                                                                                                        DB 20; Length 37;
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RESULT 14
AAY24854
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulate gastric motility and slow gastric emptying. The peptides can be used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic conditions. The peptides are exendin agonists which have activity as agents to regulate gastric motility and to slow gastric emptying, as agents to regulate gastric motility and to slow gastric emptying, as evidenced by the ability to reduce post-prandial glucose levels in mammals. They can be used for the treatment of Type I and II diabetes and hyperglycaemic or hypoglycaemic conditions. They can also be used for the treatment of disorders which would be benefited by agents which lower plasma glucose levels and in treatment of disorders which would be benefited with agents useful in delaying and/or slowing gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New exendin agonist peptides - can regulate gastric motility and slow gastric emptying, used for treating, e.g. diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY24809 to AAY24877 represent exendin agonist peptides which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Fig 4; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-394773/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              emptying.
                                                                                                                                                                                                                                                                                                    Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY24854 standard; peptide; 37
                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                Exendin agonist peptide #46.
                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-1999 (first entry)
           New exendin agonist peptides - can regulate gastric motility and slow gastric emptying, used for treating, e.g. diabetes
                                                        WPI; 1999-394773/33.
                                                                                                                                                                                                                                  WO9925727-A2.
                                                                                                                                               14-NOV-1997;
                                                                                                                                                                         13-NOV-1998;
                                                                                                                                                                                                       27-MAY-1999
                                                                                                                                                                                                                                                                Heloderma sp
                                                                                                               (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTFTSDLSKOMEBEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prickett KS;
                                                                                    Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0065442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US24210
                                                                                                                                               97US-0065442
                                                                                                                                                                             98WO-US24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.9%;
65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY24809 to AAY24877 represent exendin agonist peptides which can regulate gastric motility and slow gastric emptying. The peptides can lused for treating e.g. diabetes or hyperglycaemic or hypoglycaemic conditions. The peptides are exendin agonists which have activity as agents to regulate gastric motility and to slow gastric emptying, as avidenced by the ability to reduce post-prandial glucose levels in evidenced by the ability to reduce post-prandial glucose levels in hyperglycaemic conditions. They can also be used for hyperglycaemic conditions. They can also be used for treatment of disorders which would be benefited by agents which lower plasma glucose levels and in treatment of disorders which would be benefited with agents useful in delaying and/or slowing gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Fig 4; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11275 standard; Peptide; 37
                                         This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes; plasma glucose; gastric emptying; food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exendin agonist peptide SEQ ID NO 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB11275;
                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2000; 2000US-0116380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200041546-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-2000
                                                                                                                                                                         Example 192; Page 238; 281pp; English.
                                                                                                                                                                                                                          New formulations comprising an exendin or exendin agonist peption for increasing the sensitivity of a subject to insulin to treat
                                                                                                                                                                                                                                                                           WPI; 2000-514584/46.
                                                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                             14-JAN-1999;
                                 or reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                              L'Italien JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                 food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                               99US-0116380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%;
                                                                                                                                                                                                                                                                                                                 Kolterman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The peptides can be
                                                                                                                                                                                                                                                   peptide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Query Match

76.9%;

Score 93;

DB

21;

Length 37

Sequence

37 AA;

RESULT 16 AAB53041

AAB53041

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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia; insulin-resistance syndrome; food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extendin agonist compound #169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to extendins and their agonists which have been modified with molecular weight increasing agents such as polyethylene glycol (PEG). These can be used in the treatment of diabetes, obesity impaired glucose tolerance, postprandial dumping syndrome, postprandial hyperglycaemia, eating disorders, insulin resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-2000; 2000WO-US11814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200066629-A1
Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-672834/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMYL-) AMYLIN PHARM INC.
                                                     Amino acid sequence of an extendin agonist.
                                                                                            20-OCT-2000 (first entry)
                                                                                                                                                                 AAY94196 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTFTSALSKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                              4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                            GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0132018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%; Pred. No. 8e-10;
                                                                                                                                                                                                                                                                                                                                                     76.9%; Score 93; DB 21
68.8%; Pred. No. Be-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                       À
                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                         0,
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                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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             XXXXXXXX
                                                                                                                                                                                               AAE08427
                                                                                                                                                                                                               RESULT 18
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a modified extendin or extendin agonist. Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucagonoma; hyperglucagonemia; diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Heloderma sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1999; 99US-0116380.
30-APR-1999; 99US-0132017.
10-JAN-2000; 2000US-0175365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200041548-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4G; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
         Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                               Exendin agonist peptide #72.
                                                                                                      01-NOV-2001 (first entry)
                                                                                                                                                                           AAE08427 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                      4 GTFTSALSKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                         4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gedulin B;
                                                                                                                                                                                                                                                                                                                                                                                                                        37 AA;
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidated N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                 76.9%;
                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 21
Pred. No. 8e-10;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                      Length 37;
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                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 17 AAY94196

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Query Match Best Local Matches

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Sequence

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2001; 2001WO-US00719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200151078-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2000; 2000US-0175365
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                                               Modified-site
                                                                        Modified-site
                                                                                                 Modified-site
                                                                                                                                     Synthetic
                                                                                                                                                            Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                               Exendin agonist peptide #73.
                                                                                                                                                                                                                            01-NOV-2001
                                                                                                                                                                                                                                                    AAE08428;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 76; Page 82; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMYL-) AMYLIN PHARM INC
          WO200151078-A1
                                                                                                                                                                                                                                                                             AAE08428 standard; peptide;
                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                  4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                          GTFTSDLSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-Methyl-alanine"
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal amide"
                                                                                                              Location/Qualifiers
                                    /note= "N-Methyl-alanine; C-terminal amide"
                                                           'note= "N-Methyl-alanine"
                                                                                     'note= "N-Methyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                        76.9%;
65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 93; DB 22
Pred. No. 8e-10;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                               11;
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RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2001; 2001WO-US00719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-2000; 2000US-0175365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 77; Page 83; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                             Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
                                                                                                                                                                                                                                                                                                    Exendin agonist peptide #88.
                                                                                                                                                                                                                                                                                                                               01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                         AAE08443;
                                                                                                                                                                                                                                                                                                                                                                                AAE08443 standard; peptide; 37 AA
                                    10-JAN-2000; 2000US-0175365
                                                           09-JAN-2001; 2001WO-US00719.
                                                                                     19-JUL-2001.
                                                                                                               WO200151078-A1.
                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                  diuretic;
                                                                                                                                                                           Modified-site
                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GTXXXXXKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                              GTFTSDLSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                 coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 AA;
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young AA;
                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                       /note= "Homoproline; C-terminal amide"
                                                                                                                                                               note= "Homoproline"
                                                                                                                                                                                        note= "Homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%;
65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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WPI; 2001-514422/56

Kolterman OG,

Young AA;

(AMYL-) AMYLIN PHARM INC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretto effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride a significant effect on the reduction of blood serum triglyceride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 92; Page 92; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB64263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB64263 standard; peptide; 37
The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabetes mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished ability to increase insulin secretion. In contrast, in a normal ability to insulin resistance and insulin secretion increase. GDM pregnancy, both insulin resistance and insulin secretion increase. GDM pregnancies are associated with complications in both the mother and the foetus. Women with GDM have increased rates of Caesarian delivery, hypertensive disorders such as pre-eclampsia, and urinary tract hypertensive. GDM results in an elevated rate of foetal abnormalities such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin agonist, SEQ ID NO:83.
                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200073331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heloderma suspectum
                                                                                                                                                                                                                                          Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject,
                                                                                                                                                                                         Example 76; Page 67; 133pp; English
                                                                                                                                                                                                                                                                                              WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                                                                                       (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                           especially in a human -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTFTSDASKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                      Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           99US-0323867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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8888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC as neural tube defects, and is associated with an increased risk of CC neonatal morbidites such as hypoglycaemia, hypocalcaemia, componagnesaemia, polycythaemia, hyporalirubinaemia, and subsequent CC childhood and adolescent obesity. Exendins are peptides from the salivary CC childhood and adolescent obesity. Exendins are peptides from the salivary CC secretions of the Gila monater (exendin-4) and the Mexican beaded lizard CC (exendin-3) which exhibit homology with several members of the CC (exendin-3) which exhibit homology with several members of the CC insulinotropic effects. Unlike the compounds used to treat type 2 companies of the contraindicated for GDM, exendins and exendin CC diabetes, which are contraindicated for GDM, exendins and exendin CC agonists do not cross the placenta and thus do not cause severe prolonged CC hypoglycaemia in the newborn. They have a potent and prolonged effect on CC hypoglycaemia in the newborn. They have a potent and prolonged effect on CC weight gain, as they inhibit gastric emptying and reduce appetite. The presents a exendin agonist of the invention which is conventional incompanies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB64264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          based upon the sequence of exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB64264 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin agonist, SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB64264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator;
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WC200073331-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heloderma suspectum.
                                                                                                                                                                                                                                                                                     WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                                        Hiles R,
                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                               especially in a human
                                                                                                                                                                                                                                Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject,
                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GTFTSDLSKOMEEEÁVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                           Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                              99US-0323867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabetes mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished ability to increase insulin secretion. In contrast, in a normal pregnancy, both insulin resistance and insulin secretion increase. GDM pregnancies are associated with complications in both the mother and the foetus. Women with GDM have increased rates of Caesarian delivery, hypertensive disorders such as pre-eclampsia, and urinary tract

Example 77; Page 68; 133pp; English.

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RESULT 23
AAB64279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections. GDM results in an elevated rate of foetal abnormalities such as neural tube defects, and is associated with an increased risk of neonatal morbidites such as hypoglycaemia, hypocalcaemia, hypomagnesaemia, polycythaemia, hyporbilirubinaemia, and subsequent hypomagnesaemia, polycythaemia, hyporbilirubinaemia, and subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            based upon the sequence of exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB64279 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exendin agonist, SEQ ID NO:99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2000; 2000WO-US14231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heloderma suspectum.
ability to increase insulin secretion. In contrast, in a normal pregnancy, both insulin resistance and insulin secretion increase. GDM pregnancies are associated with complications in both the mother and the foetus. Women with GDM have increased rates of Caesarian delivery,
                                                                                                                                                     The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabete mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished to a combination of increased insulin resistance and a diminished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                                                                    Example 92; Page 75; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          especially in a human -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMYL-) AMYLIN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0323867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
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                                                                                                                                                                                                                                                        diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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8888888888888888888888888888888
                                                                    cc infections. GDM results in an elevated rate of foetal abnormalities such as neural tube defects, and is associated with an increased risk of cc as neural tube defects, and is associated with an increased risk of cc meonatal morbidites such as hypoglycaemia, hypocalcaemia, company of the Gila monster (exendin-1) and the Mexican beaded lizard company of the Gila monster (exendin-1) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the cc glucagon-like peptide family, particularly GLP-1, and have similar cc glucagon-like peptide family, particularly GLP-1, and have similar cd diabetes, which are contraindicated for GDM, exendins and exendin cc diabetes, which are contraindicated for GDM, exendins and exendin cc agonists do not cross the placenta and thus do not cause severe prolonged of plocase, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The presents as exendin agonist of the invention which is gresent sequence represents a exendin agonist of the invention which is
Sequence
                                                       based upon the sequence of exendin-4.
   37 AA;
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Matches
                                                              Query Match
                                                      Local
4 GTFTSDASKOMEEBAVRLFIEWLKNOGXSSGA 35
                     4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                            22;
                                                       Similarity
                                            Conservative
                                                         68.8%;
                                             0; Mismatches
                                                        Score 93;
Pred. No.
                                                          8e-10;
                                                                    DB 22; Length 37;
                                                 10;
                                                  0
                                                  Gaps
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RESULT 24
AAB11311
                                                                                                             AAB11311 standard; Peptide; 39 AA.
                                                                                             exendin agonist peptide SEQ ID NO 37.
                                                                                                  20-FEB-2001 (first entry)
                                                                                                        AAB11311;
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plasma glucose; gastric emptying; food intake Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;

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WO200041546-A2
                      Synthetic
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(AMYL-) AMYLIN PHARM INC

14-JAN-1999;

99US-0116380

10-JAN-2000; 2000US-0116380.

20-JUL-2000

L'Italien JJ, Kolterman 0;

WPI; 2000-514584/46.

New formulations comprising an exendin or exendin agonist for increasing the sensitivity of a subject to insulin to giaberes peptide used treat

Example 42; Figure 15; 281pp; English.

This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying or reducing food intake.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY94039 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extendin; Gila monster lizard; Mexican Beaded lizard; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of an extendin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Heloderma sp
      AAY94013-43 represent extendin agonists, derived from AAY94012. Extendins are found in the salivary glands of the Gila monster and Extendins are found in the salivary glands of the Gila monster and extending are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin a exendin for lowering plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                  14-JAN-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200041548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                          WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                                                     30-APR-1999; 99US-0132017
10-JAN-2000; 2000US-0175365.
                                                                                                                                                                               Disclosure; Fig 3B; 96pp; English.
                                                                                                                                                                                                       hyperglucagonemia and diabetes
                                                                                                                                                                                                                    Lowering plasma glucagon using exendin, an exendin agonist, exendin or a modified exendin agonist, useful for treating
                                                                                                                                                                                                                                                                                   Young A,
                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                      Gedulin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "thioproline"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "thioproline'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 11;
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. 8.5e-10;
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RESULT 26
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ID AAY94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of an extendin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY94040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY94040 standard;
         AAY94013-43 represent extendin agonists, derived from AAY94012. Extendins are found in the salivary glands of the Gila monster and mexican Beaded lizard, and have sequence similarity to glucagon-like mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin an exendin. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, useful for reacting hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                         14-JAN-1999; 99US-0116380
30-APR-1999; 99US-0132017
10-JAN-2000; 2000US-0175365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heloderma sp
                                                                                                                                                                                                                            Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-2000; 2000WO-US00942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WC200041548-A2
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                                                                                                                                                                                                                                                                                      WPI; 2000-490999/43.
                                                                                                                                                                                                Disclosure; Fig 3B; 96pp; English.
                                                                                                                                                                                                                                                                                                                Young A,
                                                                                                                                                                                                                                                                                                                                               (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 AA;
                                                                                                                                                                                                                                                                                                                   Gedulin B;
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                                                                                                                                                                                                                                                                                                                                                                                                        99US-0116380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "homoproline"
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.9%;
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Pred. No. 8
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       AAY94013-43 represent extendin agonists, derived from AAY94012. Extendins are found in the salivary glands of the Gila monster and mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic crythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of an extendin agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                Disclosure; Fig 3B; 96pp; English.
                                                                                                                                                                                                                         exendin or a modified exendin agonist, hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                          Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating
                                                                                                                                                                                                                                                                                     WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                               Young
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30-APR-1999;
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                                                                                                                                                                                                                                                                                                                 Gedulin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
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99US-0132017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-methylalanine"
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-methylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-methylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-methylalanine"
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68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39
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Pred. No. 8.5e-1
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RESULT 28
AAE08379
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                     The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and yslipidaemia, and for modifying postprandial triglyceride levels. Note: The present sequence is an agonist of exendin.

Note: The present sequence is not shown in the specification but is derived from SEQ ID NO:3 shown in page 17 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diuretic; coronary heart disease; dyslipidaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exendin agonist peptide #26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE08379 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                     Example 26; Page -; 161pp; English.
                                                                                                                                                                                             Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                  Kolterman OG,
                                                                                                                                                                                                                                                                                                                                               09-JAN-2001; 2001WO-US00719
                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2001.
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                                                                                                                                                                                                                                        WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                    10-JAN-2000; 2000US-0175365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                  Young AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Thioproline"
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Pred. No. 8.5e-10
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Query Match Best Local Similarity Watches 22; Conserv

Conservative

76.9%;

Score 93; DB 22; Pred. No. 8.5e-10; 0; Mismatches 10

10; Indels

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Gaps

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Length 39;

Sequence

39 AA;

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                                                                            Query Match
                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exendin agonist peptide #27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE08380;
                                                                                                                          The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inorropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.

Note: The present sequence is not shown in the specification but is derived from SEQ ID NO:3 shown in page 17 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                 Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2000; 2000US-0175365
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                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                    Kolterman OG,
                                                                                                                                                                                                                                                                         Example 27; Page -; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC.
                                                                                                     Sequence
                                                               POCCET
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                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA
GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35
                          GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                      39 AA;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                    Young AA;
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8
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37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Homoproline"
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                                                                76.9%;
                                                     0; Mismatches
                                                                Score 93; D
Pred. No. 8.
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                                                                                DB 22;
                                                                  Se-10;
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                                                                              Length 39;
                                                       Indels
                                                       Gaps
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RESULT 30
AAE08381
ID AAE08
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                                                    Matches
                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exendin agonist peptide #28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE08381;
                                                                                                                           The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.

The present peptide sequence is not shown in the specification but is not shown in the specification but is
                                                                                                                                                                                                                                                                            Example 28; Page -; 161pp; English.
                                                                                                                                                                                                                                                                                                    Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                      Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-2001; 2001WO-US00719.
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                        4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                 Similarity
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-Methyl-alanine"
                                                               76.98;
                                                     0
                                                    Score 93; DB 22;
Pred. No. 8.5e-10;
0; Mismatches 11
    35
                                                                              Length 39;
                                                       Indels
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Search completed: December 23, 2003, 10:01:24
Job time : 37.5 secs

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OM protein - protein search, using sw model
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Perfect score:
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2: pir2:*
3: pir3:*
4: pir4:*
XXXGTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGAXXXXX 40
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Copyright (c) 1993 - 2003 Compugen Ltd.
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A; Molecule type: protein A; Residues: 1-39 < ENG>

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ALIGNMENTS

RESULT 1

exendin-3 - Mexican beaded lizard
C.Species: Heloderma horridum (Mexican beaded lizard)
C.Species: Heloderma horridum (Mexican beaded lizard)
C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997.
C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997.
C.Accession: A23674
R.Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
J. Biol. Chem. 265, 20259-20262, 1990
A.Tible: Purification and structure of exendin-3, a new pancreatic secretagogue isolatal, Reference number: A23674; MUID:91056067; PMID:1700785
A.Reference number: A23674; MUID:91056067; PMID:1700785

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R;Eng, J.; Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P.
J. Biol. Chem. 267, 7402-7405, 1992
A;Title: Isolation and characterization of exendin-4, an exendin-3 analogue, from Helov A;Reference number: A42486; MUID:92218391; PMID:1313797
A;Accession: A42486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
HWGH4G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g in secretion of amylase. C;Superfamily: glucagon C;Superfamily: glucagon C;Keywords: amidated carboxyl end; duplication; secretagogue; venom F;39/Modified site: amidated carboxyl end (Ser) #status experimental
                                               A;Molecule type: protein
A;Residues: 1-39 <ENO>
C;Comment: Exendin-4 does not stimulate amylase secretion by pancreatic C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; venom
E;39/Modified site: amidated carboxyl end (Ser) #status experimental
                                                                                                                                                                                                                                                                                                                                                        exendin-4 - Gila monster
C;Species: Heloderma suspectum (Gila monster)
C;Species: Heloderma suspectum (Gila monster)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C;Accession: A42486
C;Accession: A42486
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75.2%; Score 91;
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     DB 1; Length 39;
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mevalonate kinase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A;Reference number: A88625; MUID:21235186; PMID:11337471
A;Accession: D86675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: D86675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: G64803; 155076
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
R;Blattner, F.R.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64803
A;Accession: G64803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphoglucomutase (EC 5.4.2.2) - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64803; I55076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-310 <STO>
                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 176, 5847-5851, 1994
A;Title: Molecular cloning and characterization of the pgm gene encoding phosphoglucomus
A;Reference number: 155076; MUID:94364967; PMID:8083177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                         A;Description: conversion of D-glucose 1-phosphate into D-glucose 6-phosphate; particips C;Superfamily: phosphoglucomutase C;Keywords: intramolecular transferase; isomerase; phosphoprotein C;Keywords:
                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-21,'M',23-546 <RES>
A;Croos-references: EMBL:U08369; NID:g473887; PIDN:AAA57067.1; PID:g473888
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE000172; GB:U00096; NID:g1786896; PIDN:AAC73782.1; PID:g1786904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown; translation not shown
                                                                                    C;Keywords: Intramorecura Common intermediate)
F;146/Active site: Ser (phosphoserine intermediate)
                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-546 <BLAT>
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52.9%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphoglucomutase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C;Accession: G85568
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A;Residues: 1-546 <8TO>
A;Cross-references: GB:AE005174; NID:g12513593; PIDN:AAG55011.1; GSPDB:GN00145; UWGP:Z
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoglucomutase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 05099 C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002 C;Accession: G90718
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C; Superfamily: phosphoglucomutase
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A;Molecule type: DNA
A;Residues: 1-546 <HAY>
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90718
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C;Superfamily: phosphoglucomutase
                                 phosphoglucomutase [imported] - Salmonella enterica subsp. enterica serovar Typhi (str C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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A;Experimental source: strain O157:H7, Bubstrain RIMD 0509952
                C; Date: 09-Nov-2001
C; Accession: AG0586
                                                                                                                                             AG0586
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DE Pred. No. 13;
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

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th, T.; Connerton, P.; Cronin, A.; Davie, F.; Davies, N., Connerton, P.; Cronin, A.; Davies, R.; Davies, N., C.; Moule, S.; C'Gaora, P.

Nature 413, 848-852, 2001

A.;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A.;Reference number: ABOSO2; MUID:21534947; PMID:11677608

A.;Accession: AGOSE6
                                                                                                                                                                        hypothetical protein SPAC26A3.17c - fission yeast (Schizosaccharomyces pombe) c;Species: Schizosaccharomyces pombe c;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T38405, T39165 R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996 A;Reference number: Z21791 A;Accession: T38405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein DR2500 - Deinococcus radiodurans (strain R1) c;Species: Deinococcus radiodurans (Strain R1) C;Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: G75266
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A; Molecule type: DNA
A;Molecule type: DNA
A;Residues: 77-57 <MCL>
A;Residues: 77-57 <MCL>
A;Cross-references: EMBL:Z69240; PIDN:CAA93240.1; GSPDB:GN00066; SPDB:SPAC26A3.17c
A;Experimental source: strain 972h-; cosmid 26A3
R;McLean, J.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR2500
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A; Residues: 1-157 < WHI>
                                                                                                                                                                                                                                                                                                                                                                                                              T38405
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Experimental source: strain R1
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13704
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A;Accession: T39165
A;Molecule type: DNA
A;Residues: 1-141 <MC2>
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C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A75001
A; Accession: A75054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; anonymous, Genoscope submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pyrococcus abyssi
C;Date: 20-Aug_1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A75054
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A;Experimental source: strain 972h-; cosmid c8E11
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                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-402 < KAW>
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                                                                                                                                                                                                                                                                                                                          Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50326.1; PID:g545
                                                                                                                                SPAC8E11.07; SPDB:SPAC26A3.17c; SPDB:SPAC8E11.11
237 KELIEEGVRVADIVVISGGASGG 259
                                                 12 KOXEEEAVRLXXXXLKNGGXSSG 34
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Similarity 34.8%;
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    Mismatches

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Pred. No. 12;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2044 <SON>
A;Cross-references: EMBL:D86546; NID:g1813375; PIDN:BAA13108.1; PID:g1813376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Sone, M.; Hoshino, M.; Suzuki, E.; Kuroda, S.; Kaibuchi, K.; Nakagoshi, H.; Saigo, Science 275, 543-547, 1997
A;Tille: Still life, a protein in synaptic terminals of Drosophila homologous to GDP-CA;Tille: Still life, a protein in Synaptic terminals of Drosophila homologous to GDP-CA;Reference number: Z17701; MUID:97153054; PMID:8999801
                                                                                                                                                                                                                                                                                                                  A; Cross-references: FlyBase: FBgn0019652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: T13704
1761 RQIIRESVRNMSIPMKNFGGSSGS 1784
                                                                         12 KOXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                  Similarity
                                                                                                                                                               Conservative
                                                                                                                                                                                         33.9%; Score 41; DB 41.7%; Pred. No. 78;
                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                    DB 2; Length 2044;
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C., Eccasion: C., Carlor R., Konster, I., Albertini, A.M., Alloni, G., Azevedo, V., Berter C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M.; Chc A., Ehrlich, S.D., Emmerson, P.T.; Entian, K.D., Errington, J., Fabret, C., Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galler iech, J., Harwood, C.R.; Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F. Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, A., Hullo, M.F. A; Authors: Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Maueel A; Authors: Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Maueel A; Anthors: Karita, A., Cudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Scanlon, A, Athors: Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Serot akeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, T., Winters, P., Wipat, A., Zumstein, E., Yoshikawa, H., Danchin, A., Rockession: C69774

A, Rockession: C69774

A, Rockession: C69774
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A;Title: Still life, a protein in synaptic terminals of Drosophila homologous to GDP-GTF A;Reference number: Z17701; MUID:97153054; PMID:8999801
A;Accession: T13707
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2064 <SON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription regulator phage-related homolog ydcN - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Z99106; GB:AL009126; NID:g2632653; PIDN:CAB12289.1; PID:g2632782
A;Experimental source: strain 168
멼
                                                                                                                                                                                                                                                                                                      A;Gene: ydcN
C;Superfamily: probable transcription repressor yowR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-127 < KUN >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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Best Local
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                                                                                                                                                                                     Match
Local Similarity 47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1781 ROIIRESVRNMSIPMKNFGGSSGS 1804
    100 EFDEETARLVKKALKNG 116
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                                                                            13 OXEEEAVRLXXXXLKNG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h
Similarity 41.7%;
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                                                                                                                                                         2; Mismatches
                                                                                                                                                                                             Score 40; DB;
Pred. No. 6.3;
                                                                                                                                                                                                                                 DB 2; Length 127;
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N;Alternate names: protein F13I12.60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 21-Jul-2000
C;Accession: T45637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-609 < CHO>
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A; Accession: T45637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: F13I12.60
C;Superfamily: beta-glucosidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: cultivar Columbia; BAC clone F13I12
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T06154
R;Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De Simone, V.; Bancroft, I.; Mewe
submitted to the Protein Sequence Database, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999 C;Accession: T06154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F24J7.162 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 215493
                                                                                                                                                                                                 A;Map position: 4
A;Introns: 4/2; 42/3; 273/2; 303/2; 342/3; 346/1; 463/3; 485/2; 536/3; 548/3; 576/3;
                                                                                                                                                                                                                                                     A;Gene: ATSP:F24J7.162
                                                                                                                                                                                                                                                                                             A; Experimental source: cultivar Columbia; BAC clone F24J7
                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-772 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T06154
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                                                                                                  Matches
                                                                                                                                                Query Match
                                                                                                                     Match 33.1%; Local Similarity 37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                              11 SKOXEEEAVRLXXXXLKNGGXSSG 34
60 SHKKEEEAKKSSSEGLKDGNAKGG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GTXXXXXSKQXEEEAVRLXXXXLKNG 29
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                                                                                                  Conservative
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                                                                                                  3; Mismatches 12; Indels
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                                                                                                                             Score 40; DB 2; Length 772; Pred. No. 43;
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Pred. No. 33;
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beta-D-glucan exohydrolase-like protein - Arabidopsis thaliana
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: D71137
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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
                                                                                                                                                                         A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29958.1; PID:g3257275
                                                        A; Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-208 <KAW>
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extracellular hypersensitive necrosis response elicitor, 34.7K - Pseudomonas syringae
C;Species: Pseudomonas syringae
C;Date: 21-Sep-1993 #semience rowinity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;He, S.Y.; Huang, H.C.; Collmer, A. Cell 73, 1255-1266, 1993
A;Title: Pseudomonas syringae pv. syringae harpinPss: a protein that is secreted via the A;Reference number: A40706; MUID:93313957; PMID:8324821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Sep-1999
C;Accession: E71845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: sequence extracted from NCBI backbone (NCBIN:135085, NCBIP:135086)
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A;Experimental source: syringae 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A,Reference number: A71800; MUID:99120557; PMID:9923682
A,Accession: E71845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyribonucleotide nucleotidyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter nvlori
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                                                                                                                                                                                                                                             A;Gene: pnp
C;Superfamily: polyribonucleotide nucleotidyltransferase alpha chain
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001541; GB:AE001439; NID:g4155724; PIDN:AAD06718.1; PID:g41557
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-688 < ARN>
                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain J99
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                                                                                                                                                            Local
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                  415 SIKNKEQVIRLVSEILESNGSSSMA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
                                                                         11 SKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TXXXXXSKQXEEEAVRLXXXXLKNG 29
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                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.2%;
                                                                                                                                                            36.0%;
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                                                                                                                                    6; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DE Pred. No. 27;
                                                                                                                                                                   Pred.
                                                                                                                                                                   Score 39; D
Pred. No. 57
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymucleotide phosphorylase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 24-Sep-1999
C;Accession: E64671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein yqbK [imported] - Lactococcus lactis subsp. lactis (strain IL1403 C;Species: Lactococcus lactis subsp. lactis C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-688 <TOM>
A;Residues: 1-688 <TOM>
A;Cross-references: GB:AE000627; GB:AE000511; NID:g2314373; PIDN:AAD08258.1; PID:g2314
C;Superfamily: polyribonucleotide nucleotidyltransferase alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E64671
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                                                                                                                                                                                                                                                   probable carbonate dehydratase (EC 4.2.1.1).- maize
N;Alternate names: probable carbonic anhydrase
C;Species: Zea mays (maize)
C;Date: Ze-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 17-Nov-2000
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A;Cross-references: GB:AE005176; PID:g12724583; PIDN:AAK05677.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471
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                                                                                                                                       R;Burnell, J.N.; Ludwig, M.; Sugiyama, T. submitted to the EMBL Data Library, April 1994
A;Description: Maize carbonic anhydrase: complementary DNAs encoding two isozymes.
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A; Residues: 1-653 < BUR >
                                                                                   A; Reference number: 214551
A; Accession: T02080
                                                                                                                                                                                                                                C; Accession:
                           A; Molecule type: mRNA
                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 32.2%; Score 39; DB 2; Local Similarity 31.2%; Pred. No. 1.5e+02;
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A;Cross-references: EMBL:U08403; NID:g606814; PIDN:AAA86945.1; PID:g606815

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K; Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.
Mol. Cell. Biol. 18, 130-140, 1998
A; Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector A; Reference number: Z17862; MUID:98078670; PMID:9418861
A; Accession: T14050
A; Accession: T14050
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T14050
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C;Keywords: ATP; phosphotransferase
C;Keywords: ATP; phosphotransferase
F;74-342/Domain: protein kinase homology <KIN>
F;1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>
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A;Residues: 1-1702 <LEU>
A;Cross-references: EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AAC02942.1
                                                                                                                                                                                                                                                                                                                                          pyrroline-5-carboxylate reductase [imported] - Agrobacterium tumefaciens (strain C58, Du C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AH2847 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-323, 2001 R; Mandale, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                  A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A,Reference number: AB2577; MUID:21608550; PMID:11743193 A,Accession: AH2847
A; Gene: proC
A; Map position:
C; Superfamily: I
                                                                                A, Experimental source: strain C58 (Dupont) C, Genetics:
                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-272 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43198.1; PID:g17740678; GSPDB:GN00186
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Superfamily: pyrroline-5-carboxylate reductase
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                               circular chromosome
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3; Mismatches
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Score 38;

DB

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Length 272;

RESULT 26

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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldma A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Biotechnology Agent Agrobacterium to A;Title: Genome Sequence of the Biotechnology Agent Agrobacterium to A;Title: Genome Agrobacterium to A;Title: Genome Sequence of the Biotechnology Agent Agrobacterium to A;Title: Genome Sequence Agrobacterium to A;Title: Genome Agrobacterium to A;Title: Genome Agrobacterium to
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E71023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushilua, W.; OhA, Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Teference number: A71000; MUID:98344137; PMID:9679194

A;Accession: E71023
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug_1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; \underline{\text{Molecule type: DNA}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sek
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                     A;Gene: PH1482 (Superfamily: transcription initiation factor IIB; transcription initiation factor II C;Superfamily: transcription initiation factor IIB; transcription initiation factor IIB homology <TF2B> F;6-291/Domain: transcription initiation factor IIB homology <TF2B>
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                                                                                                                                                                                                                        Local Similarity
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    127 KHVEEEAARLYREAVRKG 144
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                                                                                 12 KQXEEEAVRLXXXXLKNG 29
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                                                                                                                                                                                                                        31.4%; Score 38; DB 44.4%; Pred. No. 36;
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transcription initiation factor iib PAB1912 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C;Accession: E75110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 221, 199-204, 1996
A,Title: Cloning and expression of a rat brain basic helix-loop-helix factor. A,Reference number: JC4703; MUID:96220182; PMID:8660336
A;Accession: JC4703
A;Molecule type: mRNA
A;Residues: 1-357 <KAM>A;Residues: 1-357 <KAM>A;Cross-references: DDBJ:D82075; NID:g1369912; PIDN:BAA11536.1; PID:g1369913
A;Cross-references: DDBJ:D82075; NID:g1369912; PIDN:BAA11536.1; PID:g1369913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: bHLH
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4703
C;Accession: JC4703
R;Kawakami, H.; Maruyama, H.; Yasunami, M.; Ohkubo, H.; Hara, H.; Saida, T.; Nakanishi,
R;Kawakami, H.; Maruyama, H.; Yasunami, A.; 1806
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A;Experimental source: strain Orsay
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A; Residues: 1-300 < KAW>
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                                                                                                                                C;Date: 02-U11-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C;Accession: I4938; I49345
R;Lee, J.E.; Hollenberg, S.M.; Snider, L.; Turner, D.L.; Lipnick, N.; Weintraub, H.
Science 268, 836-644, 1995
Science 268, 836-644, 1995
A;Title: Conversion of Xenopus ectoderm into neurons by NeuroD, a basic helix-loop-helix
A;Title: Conversion of Xenopus ectoderm into neurons by NeuroD, a basic helix-loop-helix
                                                                         A;Reference number: A56481; MUID:95273957; PMID:7754368
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F;58-78/Region: aspartic acid/glutamic acid-rich
F;102-157/Region: helix-loop-helix #status predicted
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                                                                                                                                                                                                                                                                                                                       neurogenic differentiation factor - mouse
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                                                Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                          Species: Mus musculus (house mouse)
;Molecule type: mRNA
;Residues: 73-357 <R
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les 8; Conserv
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42.1%;
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Pred. No.
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Pred. No. 44;
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      Search completed: December 23, 2003, 10:02:38 Job time: 15.5 secs
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A;Cross-references: EMBL:U28068; NID:g854738; PIDN:AAC52203.1; PID:g854739
A;Accession: I49345
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-121 <RE3>
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C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 08-Oct-1999
C;Accession: A57059
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Genes Dev. 9, 1009-1019, 1995

A;Title: Tissue-specific regulation of the insulin gene by a novel basic helix-loop-he
A;Reference number: A57059; MUID:95293222; PMID:7774807
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                                                                                                                                                                                                                                                                                                                 R;Hammond, J.M.; Kerr, S.M.; Smith, G.L.; Dixon, L.K. Nucleic Acids Res. 20, 2667-2671, 1992
A;Title: An African swine fever virus gene with homology A;Reference number: S23018; MUID:92310959; PMID:1614852
A;Accession: S23018
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A; Residues: 1-381 <NAY>
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                                                                                                                                                                                       A;Cross-references: EMBL:X65192; NID:g58645; PIDN:CAA46310.1; PID:g58646 C;Superfamily: African swine fever virus DNA ligase C;Keywords: ATP; DNA recombination; DNA repair; ligase; phosphoprotein
                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-419 < HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 03-Mar-1994 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA ligase (ATP) (EC 6.5.1.1) - African swine fever virus C; Species: African swine fever virus, ASFV
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                                                                                                                                                                    F;151/Active site: Lys (covalent AMP-binding) #status predicted
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Length 381; Pred. No. 47;
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Pred. No. 52;
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                          NO.
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                           Score
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 December 23, 2003, 09:59:56; Search time 14.5 Seconds (without alignments)
116.720 Million cell updates/sec
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Listing first 50 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
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US-09-323-867A-99
US-09-323-867A-183
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Sequence 36,
Sequence 39,
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Sequence 21,
Sequence 23,
Sequence 26,
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Sequence 183,
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67, Appl
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184, Appl
85, Appl
85, Appl
86, Appl
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87, Appl
88, Appl
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ALIGNMENTS

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Sequence 171, Application US/09323867A Patent No. 6506724 GENERAL INFORMATION:
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                                                                                                                                                     OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2 US-09-323-867A-171
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TITLE REFERENCE: 030639.0032.UTL2 (243/131US)
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 171
                                                                                                Best
                                                                             Matches
                                                                                                               Query Match
                                                                                                                                                                                           OTHER INFORMATION:
NAME/KEY: MOD_RES
LOCATION: (36)
                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                ENGTH: 36
                                                                                                Local
                                                                             21;
                                   4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
4 GTFTSDASKOLEEBÁVŘÍFIEFÍKNGGPSSGA 35
                                                                                                    Similarity
                                                                               Conservative
                                                                                                                                                                                                                                     artificial sequence with specific variable residues
                                                                                                  76.9%;
                                                                                  0
                                                                                                    Score 93; DB 4;
Pred. No. 4.4e-10;
                                                                                    Mismatches
                                                                                        11; Indels
                                                                                                                         Length 36;
                                                                                          0
                                                                                          Gaps
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US-09-323-867A-99

Sequence 99, Application US/09323867A

Patent NO. 6506724

PATENT NOORMATION:

APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.

APPLICANT: Young, EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TILE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)

FULL REFERENCE: 030639.0032.UTL2 (243/131US)

CURRENT APPLICATION NUMBER: US/09/323,867A

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NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 183, Application US/09323867A Patent No. 6506724
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word SEQ ID NO 183
                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Young, Andrew et al.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: VARIANT
LOCATION: (36)...(37)
OTHER INFORMATION: Xaa is homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: artificial sequence with specific variable residues
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                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is N-methylalanine
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: VARIANT
                                                                                                                                                                            OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
                                                                                                                                                                                               NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                          LOCATION: (31)
OTHER INFORMATION: Xaa is N-methylalanine
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Local Similarity 68.8%;
es 22; Conservation
                                                                                              / Match 76.9%;
Local Similarity 68.8%;
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                                                                           22; Conservative
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                                      4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
GTFTSALSKOMEEEAVRLFIEWLKNGGXSSGA 35
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                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93; DB 4;
Pred. No. 4.6e-10
                                                                                                   Score 93;
                                                                                                   4.6e-10;
                                                                                                                          DB 4;
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RESULT 4 US-09-323-867A-35

Sequence 35, Application US/09323867A Patent No. 6506724

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US-09-323-867A-35
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APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032,UTL2 (243/131US)
FILE REFERENCE: 030639,0032,UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 35
                                                                                                                                                           US-09-323-867A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Applica Patent No. 6506724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1 and Microsoft Word SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Young, Andrew et al.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION. OF GESTATIONAL DIABETES
FILE REFERENCE: 036639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
                                                                                                               Query Match
                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa at position 31 is thioproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
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OTHER INFORMATION: Xaa at positions 36, 37, and 38 is thioproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 39
                                                                                                                                                                                                                                         NAME/KEY: VARIANT LOCATION: (36)...(38)
OTHER INFORMATION: Xaa at positions 36,37, and 38 is homoproline
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCATION: (39)
                                                                                                                                                                                    OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH;
                                                                                                                                                                                                          NAME/KEY: MOD_RES
LOCATION: (39)
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa at position 31 is homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                          Similarity
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                                                                         Conservative
                                                                                            76.9%;
68.8%;
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                                                                           0; Mismatches
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Pred. No. 4.8e-10
                                                                                              Score 93; DB 4;
Pred. No. 4.8e-10
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                                                                                                                         DB 4;
                                                                             10; Indels
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4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35

US-09-323-867A-39

RESULT 6

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Patent No. GOVERNATION:
GENERAL INFORMATION:
APPLICANT: AMYLIN Pharmaceuticals, Inc.
APPLICANT: AMYLIN Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
ITITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT ITITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILLE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
NUMBER OF SEQ ID NOS: 189
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; Sequence 69, Application US/09323867A
; Patent No. 6506724
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                                          Matches
                                                                                          Query Match
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TILE REPERENCE: 036639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/233,867A
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
                                                                      Best Local Similarity
                                                                                                                                                            NAME/KEY: MOD_RES
LOCATION: (35)
OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES
LOCATION: (39)
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OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa at position 31 is N-methylalanine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                             21; Conservative
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4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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68.8%;
                                                                    76.0%; Score 92; DB 4; 65.6%; Pred. No. 6.5e-10;
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Pred. No. 4.8e-10;
                                                  Mismatches
                                                                                          DB 4;
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RESULT 10

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TILLE REFERENCE: 03639, 0032, UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PATEININ Ver. 2.1 and Microsoft Word
SEQ ID NO 67
LENGTH: 36
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word SEQ ID NO 173 LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 67, Application US/09323867A Patent No. 6506724
                                                                                 Matches
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION. OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
RUMBER OF SEQ ID NOS: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MOD_RES
LOCATION: (35)
                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
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                                                                                                                                                                                 OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH
                                                                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (36)
                                                                                                  Local
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4 GTFTSDLSKOLEEEAVRLFIEFLKNGGPSSGA 35
                                       4 GTXXXXXKQXEEEAVRLXXXXLKNGGXSSGA 35
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65.6%;
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65.6%;
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                                                                                                  Score 92; DB 4;
Pred. No. 6.7e-10;
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Pred. No.
                                                                                 Mismatches
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US-09-323-867A-86
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Patent No. 6506724

GENERAL INFORMATION:

APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.

APPLICANT: Young, Andrew et al.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FLING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

SOFTWARE: Patentin Ver. 2.1 and Microsoft Word

SEC ID NO SE
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 170, Application US/09323867A Patent No. 6506724 GENERAL INFORMATION:
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LENGTH: 36
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                                                                                      Matches
                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                             LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (36)
OTHER INFORMATION: Xaa is homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: artificial sequence with specific variable residues
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                                                                                                                                                                                                                     OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD_RES LOCATION: (36)
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LOCATION: (36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
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                                                                                                           Local
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                                           4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                           76.0%;
Similarity 65.6%;
  GTFTSALSKOMEEEAVRLFIEWLKNGGPSSGA 35
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                                                                                                              Score 92; DB 4;
Pred. No. 6.7e-10;
                                                                                   Mismatches
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                                                                                        11; Indels
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Sequence 184, Application US/09323867A

Patent No. 6506724

GENERAL INFORMATION:
APPLICANT: Applicantion Pharmaceuticals, Inc.
APPLICANT: Applicantion: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
FULE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999.06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 184
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US-09-323-867A-184
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                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 65
LENGTH: 37
TYPE: PRT
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                                                                    Best
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 199-06-01
NUMBER OF SEQ ID NOS: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                           NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is Pro-NH2
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LOCATION: (36)
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                            21; Conservative
4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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                                                               76.0%;
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68.8%;
                                            0; Mismatches
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Pred. No.
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Pred. No. 6.9e-10;
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4 GTFTSDLSKOLEEEAVRLFIEFLKNGGPSSGA 35

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TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Min-
SEQ ID NO 83
LENGTH . . .
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               Query Match
Best Local S
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LENGTH: 37
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMULIS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTMARE: Patentin Ver. 2.1 and Microsoft Word
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OTHER INFORMATION: Xaa is N-methylalanine
NAME/KBY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is Pro-NH2
                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is N-methylalanine
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                                                                                                  OTHER INFORMATION: AMIDATION,
                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (37)
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LOCATION: (31)
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Conservative
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Pred. No.
                   Score 92; DB 4;
Pred. No. 6.9e-10;
                                                                                                    Position 37 is N-methylalanine-NH2
    Mismatches
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; OTHER INFORMATION: AMIDATION, Position 38 is Pro-NH2 US-09-323-867A-63
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SEQ ID NO 63
LENGTH: 38
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  Matches
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
NUMBER: OF SEQ ID NOS: 189
                                                                                                                                                                                                                                                                                                               APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
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LOCATION: (36)..(37)
COTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (37)
                                                                                                                      OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD RES LOCATION: (38)
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                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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21; Conservative
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                  % Similarity 65.6%;
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                    Score 92; DB 4;
Pred. No. 7.1e-10;
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Pred. No. 6.9e-10
                                         DB 4; Length 38;
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                                                                 US-09-323-867A-168
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; TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT
; TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
; FILE REFERENCE: 030639,0032 UTL2 (243/131US)
; CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 168
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APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TILE REPERENCE: 030639.03617122 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT APPLICATION WHOSE: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 168, Application US/09323867A Patent No. 6506724
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Best Local Similarity
                 Query Match
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                                                                                                          OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: NOD RES LOCATION: (38)
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                                                                                        OTHER INFORMATION: AMIDATION, Position 38 is Pro-NH2
                                                                                                                                                                                                                                LENGTH: 3:
TYPE: PRT
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1 Similarity 68.8%;
22; Conservation
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Pred. No. 7.1e-10;
Score 92; DB 4;
Pred. No. 7.1e-10;
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US-09-323-867A-9
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                                                                                                                                                                                                          APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TILE REFERENCE: 030639,0032,UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US(9)323,867A
CURRENT APPLICATION MAMBER: US(9)323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 9
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APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
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               LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                   NAME/KEY: MOD_RES
                                                                                             OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                     FEATURE:
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Pred. No. 7.1e-10
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Query Match

76.0%;

Score 92;

DB 4;

Length 39

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US-09-323-867A-21
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032 UTLZ (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 11
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APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMUNIS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/1310S)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILLING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
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                                                                                                           NAME/KEY: VARIANT
LOCATION: (10)
OTHER INFORMATION: Xaa is pentylglycine
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LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
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ORGANISM: Artificial Sequence
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LOCATION: (39)
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                   h 76.0%; Score 92; DB 4;
Similarity 68.8%; Pred. No. 7.3e-10;
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Pred. No. 7.
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US-09-323-867A-26
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABSTES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 26
LENGTH: 39
TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 39
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Best Local :
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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION. OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 036639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
                                                Matches
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LOCATION: (39)
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                                                                    Local Similarity
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4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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Similarity 68.6%; Pred. No. 7.3e-10
22; Conservative 0; Mismatches 1
                                              Conservative
                                                                  76.0%;
                                            0
                                                                  Score 92; DB 4;
Pred. No. 7.3e-10;
                                                Mismatches
                                                                                          Length 39;
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US-09-323-867A-30
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Patent No. 6506724
                                                                                                                                                         Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
FURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 199-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: P
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TITLE REPERENCE: 036639.0032.UTLZ (243/131US)
CURRENT APPLICATION NUMBER: US/09/233,867A
CURRENT APPLICATION NUMBER: US/09/233,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ. ID NOS: 189
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OTHER INFORMATION: Xaa at position 23 is tertiary-butylglycine
NAME/KEY: MOD RES
LOCATION: (39)

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LOCATION: (39)
OTHER INFORMATION: AMIDATION, position 39 is Ser-NH2
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                                                                                4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
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Pred. No. 7.3e-1
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Pred. No. 7.3e-10;
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US-09-323-867A-31
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APPLICANT: Amylin pharmaceuticals, Inc.

APPLICANT: Young, Andrew et al.

APPLICANT: Young, Andrew et al.

APPLICANT: Young, Andrew et al.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS

PILE REFERENCE: 030639.0032.UTL2 (244/131US)

PILE REFERENCE: 030639.0032.UTL2 (244/131US)

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

NOTWARE: Patentin Ver. 2.1 and Microsoft Word
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Patent No. 6506724
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                                                                                                                                                                                                                                                                                                    APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
FULL REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT FILING DATE: 1999-06-01
UNMBER: OF SEO ID NOS: 189
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LOCATION: (39)
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OTHER INFORMATION: Xaa at positions 36, 36, and 38 is thioproline
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               OTHER INFORMATION: Xaa at position 31 is homoproline NAME/KEY: VARIANT LOCATION: (36)..(38)
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                                                                                       NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                   OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                FEATURE:
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68.8%;
at positions 36, 37, and 38 is homoproline
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Pred. No. 7.3e-10;
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US-09-323-867A-33

OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2

OTHER INFORMATION:
NAME/KEY: MOD RES
LOCATION: (39)

Xaa

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OTHER INFORMATION: Xaa at position 31 is N-methylalanine
NAME/KEY: VARIANT
NOCATION: (36)...(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
NAME/KEY: MOD_RES
LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
US-09-323-867A-37
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Search completed: December 23, 2003, 10:04:28 Job time : 14.5~\text{secs}
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Patent No. 6506724

PATENT YOUNG, AND AIR AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS

FILE REFERENCE: 030639.0032.UTL2 (243/13)1US)

CURRENT APPLICATION NUMBER: US/09/323,867A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

SOFTWARE: Patentin Ver. 2.1 and Microsoft Word

SEQ ID NO 37

LENCTH: 39

TENCT.
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Best Local s
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: VARIANT LOCATION: (31)
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                                                                                                                                                                                                      y Match 76.0%; Score 92; DB 4; Length 39;
Local Similarity 68.8%; Pred. No. 7.3e-10;
hes 22; Conservative 0; Mismatches 10; Indels
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OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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188.107 Million cell updates/sec
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Match Length DB
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  SwissProt_41:*
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DNLI ASEM2
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BIOF AQUAE
CDXP BRAJA
FLY TOBAC
XYLA ARATH
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1_DROME
3_HUMAN
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Q9v0v5 pyrococcus
059151 pyrococcus
060430 mesocricetu
060867 mus musculu
064289 rattus norv
266813 african swi
004973 lycopersico
p39945 saccharomyc
                                                                      P23648 lactococcus
Q9uhy8 homo sapien
P97578 rattus norv
O87389 rhizobium m
P20497 vaccinia vi
   066875
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P15715
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O14682 homo sapien
O35709 mus musculu
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P26349 heloderma s
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                                    P33059 variola vir
O66875 aquifex aeo
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     arabidopsis rhizobium m
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HSSP; P01275; 1BH0.
InterPro; IPR000532; Glucagon.
Pfam; PF00123; hormone2; 1.
SMART; SM00070; GLUCA; 1.
SMORTE; PS00260; GLUCAGON; 1.
PROSITE; PS00260; GLUCAGON; 1.
Glucagon family; Toxin; Amidation.
MOD RES
39
SEQUENCE 39 AA; 4204 MW; A44251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P20394;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91056067; PubMed=1700785;
Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman J.-P.;
"Purification and structure of exendin-3, a new pancreatic
secretagogue isolated from Heloderma horridum venom.";
J. Biol. Chem. 265:20259-20262(1990).
-I- FUNCTION: Has a VIP/secretin-like biological activity. Interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heloderma horridum horridum (Mexican beaded lizard).
Heloderma horridum korridum (Mexican beaded lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8552;
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                                                                                                                                          21;
                                                      4 GTXXXXXSKQXEEBAVRLXXXXLKNGGXSSGA 35
   4 GTFTSDLSKOMEEEAVRLFIEWLKNGGPSSGA
                                                                                                                                                                                 Similarity
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                 75.2%;
65.6%;
                                                                                                                                              0
                                                                                                                                                                             Score 91; DB 1;
Pred. No. 6.6e-10;
                                                                                                                                                                                                                                                                                         A44251D3A4B1D1B9 CRC64;
                                                                                                                                                                                                                                                                                                                                    AMIDATION
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EXE4 HELSU ID EXE4 HELSU AC P26349; DT 01-MAY-1992 DT 15-JUL-1998

STANDARD;

87 AA

P26349; 01-MAY-1992 15-JUL-1998

(Rel. 22, Created)
(Rel. 36, Last sequence update)

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Heloderma suspectum (Gila monster).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.";
J. Biol. Chem. 272:4108-4115(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eng J., Kleinman W.A., Singh L., Singh G., Raufman J.-P.; "Isolation and characterization of exendin-4, an exendin-3 analogue, from Heloderma suspectum venom. Further evidence for an exendin receptor on dispersed acini from guinea pig pancreas."; J. Biol. Chem. 267:7402-7405[1992].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 267:7402-7405(1992).
-!- FUNCTION: Has a VIP/secretin-like biological activity. Interacts
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Expressed by the venom gland.
-!- TISSUE SPECIFICITY: Expressed by the FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Y.E., Drucker D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97172477; PubMed=9020121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92218391; PubMed=1313797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 48-86.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                 01-JUN 1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A42486; HWGH4G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U77613; AAB51130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000532; Glucagon.
NCBI_TaxID=562;
                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                   SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                   MOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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SMART; SM00070; GLUCA; 1.
                   Enterobacteriaceae;
                                                 Escherichia coli
                                                                                                                                                                  ECOLI ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                               ucagon family; Toxin; Amidation; Signal; 3D-structure.
                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                 4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                GTFTSDLŚKOMEĖĖAVRLFIEWLKNGGPSSGA
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                                                                               ucomutase
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                    9479 MW;
                      Escherichia
                                                                                                                                                                                                                                                                                                                                   75.2%;
65.6%;
                                                                                                                                                                                                                                                                                                                                                     Score 91;
                                                                                                                                                                                                                                                                                                                                                                                    656BA6E3D87454A2 CRC64;
                                                                                                                                                                                                                                                                                                                                       Pred
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                                                                                                                                                                                                                                                       82
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        InterPro; IPR005841; PG/PMM_mutage.
InterPro; IPR005844; PG_PMM_ABAII.
InterPro; IPR005845; PG_PMM_ABAII.
InterPro; IPR005846; PG_PMM_ABAIII.
InterPro; IPR005846; PG_PMM_C.
InterPro; IPR005843; PG_PMM_C.
InterPro; IPR005852; Pgliccomut_A.
Pfam; PF00408; PGM_PMM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and characterization of the pgm gene encoding phosphoglucomutase of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94364967; PubMed=8083177
                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.ish.ci.
                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphoglucomutase from Escherichia coli.";
J. Biol. Chem. 239:2741-2751(1964).
- FUNCTION: THIS ENZYME PARTICIPATES IN BOTH THE BREAKDOWN AND
- SYNTHESIS OF GLUCOSE
- CATALYTIC ACTIVITY: Alpha-D-glucose 1-phosphate = alpha-D-glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SegA: a negative modulator Cell 77:413-426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94236686; PubMed=8011018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-20 FROM N.A.
                                                                                                                                         EcoGene; EG121
                                                                                                                                                                                                                         EMBL; AE000172;
                                                                                                                                                                                                                                       EMBL; U08369; AAA57067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphoglucomutase. II. Purification and properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 176:5847-5851(1994)
                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
                                                                                                                                                           G64803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kleckner N.;
                                                                                                                                                                                         D90708; BAA35345.1;
                                                                                                                                                                                                       D90707; BAA35337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Handler P.;
                                                                                                                                                             G64803
          PGM_PMM_I; 1
                                                                                                                                                                                                                            AAC73782.1; -.
                                                                                                                                                                         NOT ANNOTATED CDS
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Pfam; PF02880; PGM PMM III; 1.
TIGRPAMS; TIGR01132; PGM; 1.
PROSITE; PS07710; PGM_PMM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties."!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation its buropean Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97368292; PubMed=9223287;
Irwin D.M., Satkunarajah M., Wen Y., Brubaker P.L., Pederson R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=042143-2; Sequence=VSP_001755;
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                    EMBL; AF004432; AAB65660.1; -. HSSP; P01274; IGCN.
                                                                                                                                                                                                                       Interpro; IPR000532; Glucagon. pfam; pF00123; hormone2; 5.
                                                                                       PROSITE; PS00260; GLUCAGON; 5.
Glucagon family; Hormone; Signal; Cleavage on pair of basic residues;
Glucagon family; Alternative splicing.
  PEPTIDE
PROPEP
                                                                                                                                                                                                 PRINTS;
                                                                            SIGNAL
                                                  PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 KOIEKEAVEIVSEVLKN 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the blood sugar level.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=042143-1; Sequence=Displayed
                                                                                                                                                                         ; PR00275; GLUCAC
SM00070; GLUCA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546 AA; 58361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tropic properties.";
21. Acad. Sci. U.S.A. 94:7915-7920(1997).
TION: Promotes hydrolysis of glycogen and lipids, and raises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                       GLUCAGON.
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Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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YAUH_SCHPO
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PEPTIDE
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Q10170; Q9Y717;
Q10170; C9Y717;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C26A3.17C in chromosome
Hypothetical protein C26A3.17C in chromosome
SPAC26A3.17C OR SPAC8E11.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                    -!- SIMILARITY: SOME, TO RAT GUANIDINOACETATE N-METHYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GTFTSDVTQQLDEKAAKEFIDWLINGGPS 128
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 2).
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RESERVATE RESERV
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A RICHARDS B. F., Jordan H., Moore T., A.A., Rubin G.M., Schuler G.D., Altschil S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschil S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschil S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschil S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Diatchenko L., Marusina K., Farmer S., Caroinci P., Prange C., Staplecon M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Caroinci P., Prange C., Andrew G., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J., Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Andrew G., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Va Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Best Local
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EMBL; Z69240; CAA93240.1; -.
GeneDB SPOMDe; SPAC26A3.170; -.
InterPTO; IPR002110; ANK.
IPR051TE; PS50297; ANK. REP_REGION; UNKNOWN_1.
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014682; 075464; Q9UPG9;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ectoderm-neural cortex-1 protein (ENC-1) (P53-
(Nuclear matrix protein NRP/B).
ENC1 OR PIG10 OR NRPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 357 AA; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hernandez M.-C., Andres-Barquin P.J., Holt I., Israel M.A "Cloning of human ENC-1 and evaluation of its expression regulation in nervous system tumors."; Exp. Cell Res. 242:470-477(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Colon cancer;

MEDLINE=97449378; PubMed=9305847;

Polyak K., Xia Y., Zweier J.L., Kinzler K.W., Vogelstein Polyak K., Taia Y., Zweier J.L., Kinzler K.W., Vogelstein "A model for p53-induced apoptosis.";

Nature 389:300-305(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98350113; PubMed=9683534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "NRP/B, a novel nuclear matrix protein, associates with p110(RB) and is involved in neuronal differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell Biol. 141:553-566(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota S., Raja S., Rogers R., Rivnay B., Avraham H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40709 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB : Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5529B8D3B88D91A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (P53-induced protein 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Israel M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 5.
SMART; SM00225; BTB; 1.
SMART; SM00612; Kelch; 6.
PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                 EMBL; AF059611; AAC26109.1; -.
EMBL; BC000418; AAH00418.1; -.
Genew; HGNC:3345; ENC1.
                                                                                                                                                                                                                                                                                                                                              EMBL; AF010314; AAC39532.1; -. EMBL; AF005381; AAC64498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -|- SIMILARITY: Contains 1 BTB/POZ domain.
                                       CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; TAS.
GO; GO:0007275; P:development; T
GO; GO:0007399; P:neurogenesis;
                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        InterPro; IPR000210; BTB
InterPro; IPR006652; Kelc
 SEQUENCE
                                                                                                                                                                                 Repeat;
                                                                                                                                                                                         Actin-binding; Developmental protein; Cytoskeleton; Kelch repeat;
                                                                                                   CONFLICT
                                                                                                                        REPEAT
                                                                                                                                           REPEAT
                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                        605173;
                                                                                                                                                                                Phosphorylation.
  589
  Ã,
                                                                                                                                                      388
  66129 MW;
                                                                                                                                                                                                                                                         Kelch_rep
                                                                                                                                                                                                                                                                   POZ.
RL -> TR (IN REF. 2).
C -> S (IN REF. 1).
V -> A (IN REF. 1).
LREGVSNAA -> RPRRRYNCAQ (IN REF. 1).
LREGVSNAA -> RPRRRYNCAQ (IN REF. 1).
YTAAAVLGNQIFIMGGDTEFSACSAYKFNSETYQMTKVGDV
TAKRMSCHAVASCHKLYVGGYFGIQRCKTLDCYDPTLDVM
NSITTVPYSLIFTAFVSTWKHLPS -> IHSQASCPGGTQD
TT WGVIONFSACCCL (IN REF. 1).
                                                                                                               KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 6.
                                                                                WSFK (IN REF. 1).
RL -> TR (IN REF. 1).
                                                                                                      INEENAESLLEAGDMLEFQ ->
                                                                                                       HQLEGKCRNSLLGSLVTC
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Query Match Best Local S Matches

Similarity 9; Conser

Conservative

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Mismatches

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Gaps

0

33.9%; 45.0%;

Score 41; DE Pred. No. 11;

ВВ

Length 589; Indels

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11

SKOXEEEAVRLXXXXLKNGG 30

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밁
 Best Local Similarity
Matches 9; Conser
                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENC1 MOUSE
035709;
16-0CT-2001
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Swiss albino; TISSUE=Brain; MEDLINE=97252647; PubMed=9096139; Hernandez M.-C., Andres-Barquin P.J., Martinez S., Bulfone A., Rubenstein J.L.R., Iszael M.A.; "ENC-1: a novel mammalian kelch-related gene specifically expressed in
                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the nervous system encodes an actin-binding protein.";
J. Neurosci. 17:3038-3051(1997).
-!- FUNCTION: ACTIN-BINDING PROTEIN INVOLVED IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ectoderm-neural cortex-1 protein (ENC-1).
ENC1 OR ENC-1
                                                                                                                                                                          SMART; SM00225; BTB; 1.
SMART; SM00612; Kelch; 6.
                                                                                                                                                                                               Pfam; PF00651; BTB; 1.
Pfam; PF01344; Kelch; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENC1 OR ENC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                              SEQUENCE
                                                                                  REPEAT
                                                                                            REPEAT
                                                                                                       REPEAT
                                                                                                                                                                                                                       InterPro; IPR000210; BTB_POZ.
InterPro; IPR006652; Kelch_rep.
                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 6 Kelch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                    REPEAT
                                                                                                                               DOMAIN
                                                                                                                                                   Actin-binding; Developmental
                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                          CYTOSKELETON.
TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN THE NERVOUS SYSTEM.
DEVELOPMENTAL STAGE: EXPRESSION IS HIGHLY DYNAMIC BUT MOSTLY
DEVELOPMENTAL STAGE: EXPRESSION IS DETECTED IN
RESTRICTED TO THE NS. OUTSIDE THE NS. EXPRESSION IS DETECTED IN
THE ROSTRAL-MOST SOMITOMERE OF THE PRESOMITIC MESODERM, AT THE
TIMES CORRESPONDING TO THE EPITHELIALIZATION THAT PRECEDES SOMITE
FORMATION. FIRST DETECTED IN THE BRAIN AND SPINAL CHORD OF 12 PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC. INTERACTS WITH THE ACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEURONAL PROCESS FORMATION AND IN DIFFERENTIATION OF NEURAL
                                                                                                                                                                                                                                              MGI:109610; Encl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262
                                                                                                                                                                                                                                                          U65079; AAB64206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEIVEEAIRCKLKILQNDG 281
                                                                                                                                                                 PS50097;
                                              589
                                                                                296
341
389
  Conservative
                                              A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                 BTB; 1.
                                                                                 444
492
                                                                                                      114
340
388
                                              66085 MW;
33.9%; Score 41; DB 1; Length 589;
45.0%; Pred. No. 11;
tive 3; Mismatches 8; Indels
                                                                    HELLOH
KELCH
KELCH
KELCH
KELCH
                                                                                                                                                     protein; Cytoskeleton; Kelch repeat;
                                                          KELCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                              12E62354D508B6A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 AA.
<u>.</u>.
Gaps
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RESULT
SIF2_DR
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FlyBase; FBgn0019652; sif.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001448; PDZ.
InterPro; IPR001849; PH.
InterPro; IPR003116; RBD.
InterPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIF2_DRC
P91620;
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H., Saigo K., Nabeshima Y.-I., Hama C.; Science 275:1405-1405 (1997).

-!- FUNCTION: RECULATES SYNAPTIC DIFFERENTIATION THROUGH THE ORGANIZATION OF ACTIN CYTOSKELETON POSSIBLY BY ACTIVATING RHO-LIKE ORFPASSES. IS LIKELY A FACTOR IN THE CASCADE OF RAC1 OR CDC42 IN THE UNITED CONTROL
                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DROME
                                                                                                                                                                                                                           EMBL; D86546; BAA13108.1; -. PIR; T13704; T13704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Still life, a protein in symaptic terminals of Drosophila homologous to GDP-GTP exchangers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sone M., Hoshino M., Suzuki E., Kur
Saigo K., Nabeshima Y.-I., Hama C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Still life protein type 2 (SIF type 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
-!- SIMILARITY: Contains 2 PH domains.
-!- SIMILARITY: Contains 1 Ras-binding (RBD) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97153054; PubMed=8999801;
Sone M., Hoshino M., Suzuki E., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 275:543-547(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOId=P91621-1; Sequence=External;
DEVELOPMENTAL STAGE: AT STAGE 14, EXPRESSION OCCURS IN EACH
SEGMENT OF THE CENTRAL NERVOUS SYSTEM. AT STAGE 17, EXPRESSION
BECOMES RESTRICTED TO THE SYNAPTIC REGIONS OF THE BRAIN AND
VENTRAL NERVE CORD, WHERE SYNAPSES UNDERGO MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: LOCALIZES TO THE SUBMEMBRANOUS REGION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=SIF type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=SIF type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNAPTIC TERMINALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 SKEIVEEAIRCKLKILQNDG
                                                                                                                                                                                                   P08567; 1PLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P91620-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
SIF1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00233; PH; 2.
SMART; SM00455; RBD; 1.
SMART; SM00325; RBDGEF; 1.
SMART; SM00325; RBOGEF; 1.
PROSITE; PS00741; DH 1; 1.
PROSITE; PS50106; PD 2; 1.
PROSITE; PS50106; PD 2; 1.
PROSITE; PS50106; PD DMAIN;
                                                                                                                                                                                                                                                                                                                                                      SIF1 DROME
P91621;
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00228; PDZ; 1
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guanine-nucleotide releasing factor; Developmental protein; Synapse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Alternative DOMAIN 62 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02196; RBD; 1.
Pfam; PF00621; RhoGEF; 1.
                               Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H., Saigo K., Nabeshima Y.-I., Hama C.; Science 275:1405-1405((1997).

-!- FUNCTION: REGULATES SYNAPTIC DIFFERENTIATION THROUGH THE ORGANIZATION OF ACTIN CYTOSKELETON POSSIBLY BY ACTIVATING RHO-LIKE GREASES. IS LIKELY A FACTOR IN THE CASCADE OF RAC1 OR CDC42 IN THE
                                                                                                                                MEDLINE=97153054; PubMed=8999801;
Sone M., Hoshino M., Suzuki E., Kuroda S., Kaibuchi K., Nakagoshi H.,
Saigo K., Nabeshima Y.-I., Hama C.;
"Still life, a protein in synaptic terminals of Drosophila homologous
to GDP-GTP exchangers.";
Science 275:543-547(1997).
                                                                                                                                                                                                                                                        Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50898; RBD;
                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence u. 28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                    Still life protein type 1 (SIF type 1).
                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              1761 ROIIRESVRNMSIPMKNFGGSSGS 1784
          SUBCELLULAR LOCATION: LOCALIZES TO THE SUBMEMBRANOUS REGION OF
SYNAPTIC TERMINALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 KOXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.9%;
Similarity 41.7%;
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819
1101
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                                                                                                                                                                                                                                                                                                                                            Last sequence update)
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DH.
PH 2.
POLY-PRO.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75D7CF21F49654B6 CRC64;
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Best Local
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InterPro; IPR001478; PDZ.
InterPro; IPR0011649; PH.
InterPro; IPR001316; RBD.
InterPro; IPR000219; RhoGEF.
InterPro; IPR001960; WH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comenties requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOId=P91620-1; Sequence=External;
-!- DEVELOPMENTAL STAGE: AT STAGE 14, EXPRESSION OCCURS IN EACH SEGMENT OF THE CENTRAL NERVOUS SYSTEM. AT STAGE 17, EXPRESS BECOMES RESTRICTED TO THE SYNAPTIC REGIONS OF THE BRAIN AND VENTRAL NERVE CORD, WHERE SYNAPSES UNDERGO MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=SIF type 1;
                                                                                                                                                                                                                                                                                                                               SMART; SM00325; RhoGEF; 1.
SMART; SM00461; WH1; 1.
PROSITE; PSS00741; DH 1; 1.
PROSITE; PSS0010; DH 2; 1.
PROSITE; PSS0106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
-!- SIMILARITY: Contains 2 PH domains.
-!- SIMILARITY: Contains 1 Ras-binding (RBD) domain.
                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00228; PDZ;
SMART; SM00233; PH; 2
SMART; SM00455; RBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00169; PH; 1.
Pfam; PF02196; RBD; 1.
Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D86547; BAA13109.1; -. PIR; T13707; T13707. HSSP; P08567; 1PLS.
                                                                                                                       DOMAIN
LIPID
                                                                                                                                                                                                                                                                                                     PROSITE; PS50106; PDZ; PROSITE; PS50003; PH DO PROSITE; PS50898; RBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0019652; sif
                                                                                                                                                                                                                                                                                       Guanine-nucleotide
                                                                                                           SEQUENCE
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                            Myristate;
                                                                                                                                                    DOMAIN
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 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P91621-1; Sequence=Displayed;
                          12 KOXEEEAVRLXXXXLKNGGXSSGA 35
                                                                   Similarity
ROITRESVRIMSIPMKNFGGSSGS 1804
                                                                                                                                                                                                                                                              Synapse;
839 s
                                                                                                                                      1121
1204
1428
1694
445
545
1315
1315
1918
                                                                                                           2064
                                                     Conservative
                                                                                                           AA,
                                                                                                                                                                                                                                                                                       releasing factor; Developmental protein; Repeat;
                                                                                                                                                                                                                                                                          Alternative splicing.
                                                                                                                                                                                                                                                                                                                   DOMAIN; 1.
                                                                   41.7%;
                                                                               33.9%;
                                                                                                           230489 MW;
                                                     ; Score 41; DB; Pred. No. 42; 4; Mismatches
                                                                                                                                                   POLY-GLN.
POLY-GLN.
                                                                                                                                                                                           PH 2.
POLY-GLY.
                                                                                                                           MYRISTATE
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                                                                                                                                       POLY-PRO.
                                                                                                             D3BDCC10A94D9E6C CRC64;
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                                                                                                                           (POTENTIAL)
                                                                                 DB 1; Length 2064;
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                                                         0
                                                         Gaps
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RESULT 10 TRL3_HUMAN ID TRL3_HUMAN

STANDARD;

1017 AA

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RESULT 11
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01-JUN-1994
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which
code for large proteins in vitro.";
DNA Res. 7:273-281(2000).
-!- FUNCTION: MAY BE A CALCIUM CHANNEL.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                              SEQUENCE FROM N.A., AND SEQUENCE
                                                                                                                                                 ?seudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                               Harpin-PSS
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P35674;
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MEDLINE=93313957;
                                                                                                                              Pseudomonadaceae;
                                                                                                                                                                                                         HRPZ
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                                                                                                   _TaxID=321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129
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IPR005821; Ion_trans.
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(Rel.
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. 29, Last sequence 37, Last anno
PubMed=8324821
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Pred. No. 30;
4; Mismatches
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                                                                                                                                                    Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; "An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512 (2003).

11. Microbiol. 47:1495-1512 (2003).

12. ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLAN UPON INFECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO REQUIRED FOR PATHOGENICITY IN HOST.
-!- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.
-!- MISCELLANEOUS: DIFFERENT PLANTS EXHIBIT DIFFERENT LEVELS OF SENSITIVITY TO HARPIN-PSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      He S.Y., Huang H.-C., Collmer A.; "Pseudomonas syringae pv. syringae harpinPss: a protein that is secreted via the Hrp pathway and elicits the hypersensitive response
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Cell 73:1255-1266(1993)
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                              PubMed=12622808;
Cohen G.N., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRAB
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                                                                       INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to the TFIIB family.
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GE5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TF2B_PYRAB
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EMBL

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RESULT 13
TF2B_PYRHO
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InterPro; IPR006670; Cyclin.

InterPro; IPR0080812; TFIIB euk.

InterPro; IPR008812; Traiscript_Tac2; 2.

Pfam; PF00382; transcript_Tac2; 2.

PRINTS; PR00685; TIFACTORIIB.

SMART; SM00385; CYCLIN; 2.

PROSITE; PS00782; TFIIB; 2.
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                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98344137; PubMed-9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Takamiya M., Ohfuku Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transcription initiation factor IIB (TFIIB).
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059151;
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nes 8; Conserv
                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                              COFACTOR: Binds 1 zinc ion per subunit (By similarity). SIMILARITY: Belongs to the TFIIB family.
                                                                                                                                                                                                                                                                                             Res. 5:55-76(1998).
FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A
ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO
                                                                                                                                                                                                                                 INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY)
COFACTOR: Binds 1 zinc ion per subunit (By similar
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Pred. No.
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01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Neurogenic differentiation factor 1 (NeuroD1)
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                                                                                                                                                                                                              MEDIINE=95293222; PubMed=7774807;
Naya F.J., Stellrecht C.M.M., Tsai M.-J.;
"Tissue-specific regulation of the insulin gene helix-loop-helix transcription factor.";
Genes Dev. 9:1009-1019(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDF1
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ZN_FING 7
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InterPro; TPR006670; Cyclin.
InterPro; TPR008812; TFIIB euk.
InterPro; Pranscript_Fac2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00383; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; E71023; E71023.
                                                                                                                                                                                                                                                                                                                                                                                                                                       activator 2) (BETA2)
NEUROD1 OR NEUROD
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                                                                                                                                                                                                                                                                                                                                                                                               Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN, HETERODIMER WITH E47.
SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: MOST ABUNDANT IN PANCREATIC ALPHA- AND BETA-CELLS, LESS IN BRAIN AND INTESTINE.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P29095; 1AIS.
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                                                                                                                                                                                                                                                                                                                                                  TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRODGES; TIPHLAND PRODGES; CYCLIN; 2. meno782; TFIIB; 2.
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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ZINC
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Pred. No. 20;
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     war outstation -
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                            helix-loop-helix protein.";
Science 268:836-844(1995).
-:- FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.
-:- TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.
-:- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BILLH PROTEIN. HETERODIMER WITH E47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
DNA-binding; Nuclear protein;
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDF1 MOUSE STANDARD; PRT; 357 AA. Q60867; Q60897; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neurogenic differentiation factor 1 (Neurobl). NEURODI OR NEUROD.
          GO; GO:0001654; P:eye morphogenesis; IMP. InterPro; IPR001092; HLH_basic.
                                     EMBL; U28068; AAC52203.1; -.
EMBL; U28888; AAC52204.1; -.
PIR; I49338; I49338.
MGD; MGI:1339708; Neurod1.
                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      Lee J.B., Hollenberg S.M., Snider L., Turner Weintraub H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=MF1, and 129/Sv; MEDLINE=95273957; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                                                                                          "Conversion of Xenopus ectoderm into neurons by NeuroD, a basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090
                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear (Potential).
TISSUE SPECIFICITY: EXPRESSED IN DIFFERENTIATING NEURONS OF BOTH THE CENTRAL AND PERIFHERAL NERVOUS SYSTEMS.
DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYONIC DEVELOPMENT.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FANTRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIND
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58 77 GJU-RICH (ACIDIC).

86 92 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)

01 112 BASIC DOMAIN.

13 153 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).

67 75 POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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Rodentia;
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42.1%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                             (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                   a collaboration
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EMBL; D82075; BAA11536.1; -. EMBL; D82074; BAA11535.1; -. EMBL; U80603; AAB38744.1; -. EMBL; U74703; JC4703.

moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/

restrictions on EMBL

50

outstation

nterPro;

IPR001092; HLH_basic

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RESULT 16
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Best Local
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic differentiation factor 1 (NeuroD1) (Effector 1) (BHF-1).
NEUROD1 OR NEUROD.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Rodentia; Sciurognathi; Muri
                                                                                                                                                                                      Ahmad I., Acharay H.R.;

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: ACTS AS A DIFFERENTIATION FACTOR DURING NEUROGENESIS.

-i- TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INSULIN GENE E-BOX.

SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. HETERODYNER WITH E47.

-i- SUBCELLULAR LOCATION: Nuclear (Potential).

-i- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; TISSUE=Retina; Ahmad I., Acharay H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawakami H., Maruyama H., Yasunami M., Ohkubo H., Hara H., Saida
Nakanishi S., Nakamura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q64289;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurogenesis;
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PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 88-200 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakanishi S., Nakamura S.;
"Cloning and expression of a rat brain basic helix-loop-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96220182; PubMed=8660336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tactor
                                                                                                                                                                            TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
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357 AA;
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87
102
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58 77 GLU-RICH (ACIDIC).
87 93 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39998
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POLY-LYS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             221:199-204(1996)
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                                                                                                                       a collaboration - MBL outstation
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Best Local
                  EMBL; X65192; CAA46310.1; -.
EMBL; X71982; CAA50805.1; -.
PIR; S23018; S23018.
InterPro; IPR000977; DNA_ligase.
Pfam; PF01068; DNA_ligase.
Pfam; PF010697; DNA_LIGASE_A1; 1.
PROSITE; PS00033; DNA_LIGASE_A2; 1.
PROSITE; PS00333; DNA_LIGASE_A3; 1.
PROSITE; PS00333; DNA_LIGASE_A3; 1.
PROSITE; PS00160; DNA_LIGASE_A3; 1.
PROSITE; PS00160; DNA_LIGASE_A3; 1.
PROSITE; PS00160; DNA_LIGASE_A3; 1.
PROSITE; PS00160; DNA_LIGASE_A3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
DNA ligase (BC 6.5.1.1) (Polydeoxyribonucleotide synthase [ATP]).
African swine fever virus (isolate Malawi Lil 20/1) (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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DOMAIN 58 77 GLU-RICH (ACIDIC).

DOMAIN 87 93 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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PROSITE; PS00038; HLH 1; 1.

PROSITE; PS50888; HLH_2; 1.

DNA-binding; Nuclear protein; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92310959; PubMed=1614852;
Hammond J.M., Kerr S.M., Smith G.L., Dix
"An African swine fever virus gene with
Nucleic Acids Res. 20:2667-2671(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASFM2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dixon L.K., Twigg S.R.F., Baylis S.A., Vydelingum S., Bristow C., Hammond J.M., Smith G.L.;
"Nucleotide sequence of a 55 kbp region from the right end of the genome of a pathogenic African swine fever virus isolate (Malawi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P26813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94292916; PubMed=8021596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNLI_ASFM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JIL20/1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gen. Virol. 75:1655-1684(1994).

FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION, DNA FUNCTION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA. RECOMBINATION AND DNA REPAIR REPLICATION AND RECOMBINATION. IT IS NOT ESSENTIAL FOR VIRAL REPLICATION AND RECOMBINATION. CATALYTIC ACTIVITY: ATP + (deoxyribonucleotide) (M) = AMP + diphosphate + (deoxyribonucleotide) (M) = AMP + diphosphate + (deoxyribonucleotide) (N+M).

- SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.
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   repair;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KOXEEEAVRLXXXXLKNGG 30
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8; Conserv
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   DNA replication;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY)
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      DNA
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      recombination;
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            Cell
         division; Ligase;
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Best Local
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                                                                                               Matches
                                                                                                                                                 Query Match
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Spermatophyta; Magnoliophyta; eudicotyledons; core et
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sepence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-isopropylmalate synthase A (EC 2.3.3.13) (A
synthase A) (Alpha-IPM synthetase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       004973;
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BINDING 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                               PROSITE; PS00815; AIPM HOMOCIT SYNTH 1; 1.

PROSITE; PS00816; AIPM HOMOCIT SYNTH 2; FALSE NEG.

Leucine biosynthesis; Transferase.

SEQUENCE 589 AA; 64360 NW; 150E48900188BDDF CR
                                                                                                                                                                                                                                                                                                  InterPro; IPR002034; AIPM/Hcit_synth.
InterPro; IPR008091; HmGL-like.
InterPro; IPR005671; LeuA_bact.
Pfam; PF00682; HmGL-like; 1.
TIGRFAMS; TIGR00973; leuA_bact; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=28526;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF004165; AAB61598.1;
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                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 SVKNEDEALRIKTOFIKEG 289
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40
                                                 11 SKOXEEEAVRLXXXXLKNGGXSSGA 35
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8; Conser
                                                                                               Similarity
9; Conserv
SKISDPKYVRIFDTTLRDGEQSPGA
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                                                                                                                              36.0%;
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMP
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                                                                                                                                                    Score 38;
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                                                                                                                                                      DB 1; Length 589;
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Best Local
STRAIN-Bristol N2;
MEDLINE-94150718; PubMed=7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Co
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metaroa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKT1_CAI
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"The nucleoide sequence of Saccharomyces cerevisiae chromosome V."; Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U18839; AAB64656.1; -.
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                                                                                                                                                                                                                                                                                                                                                                            VCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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15-SEP-2003 (Rel.
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$5000993; AST2.
; $0000993; C:cytoplasm; IDA.
;GO:0005737; C:cytoplasm; IDA.
;erPro; IPR002085; Adh zn family.
am; PF00107; ADH zinc N; I.
am; PF00107; ADH zinc N; FBEC2F2CDE894F84 CRC64;
an; PF00107; ADH Zinc N; FBEC2F2CDE894F84 CRC64;
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38-1994 (Rel. 28, Last sequence update)
39-2003 (Rel. 42, Last annotation updat)
40 (Rel. 42, Last annotation updat)
41 (Rel. 42, Last annotation)
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Pred. No.
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Best Local :
"CDNA cloning and complete primary structure of skeletal muscle phosphorylase kinase (alpha subunit).", proc. Natl. Acad. Sci. U.S.A. 85:2929-2933(1988).
                                                                                                                                                                                                                                            KPB1 RABIT STANDARD; PRT; 1237 AA. P18688; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) phosphorylase B kinase alpha regulatory chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                          TISSUE-Skeletal muscle;
MEDLINE-88203614; PubMed-3362857;
MEDRINE-88203614; PubMed-3362857;
Zander N.F., Meyer H.E., Hoffmann-Posorske
Heilmeyer L.M.G. Jr., Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                     PHKA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                              NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                lsoform (Phosphorylase kinase alpha M subunit)
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HSSP; P23807; 1IXX.
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nterPro; IPR001304; Lectin_C.
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N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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(See http://www.isb-sib.ch/announce/
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                                                                E., Crabb J.W.,
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PIR; A31334; A31334.
Glycogen metabolism; Muscle; Phosphorylation; Calmodulin-binding;
Alternative splicing; Multigene family.
DOMAIN 810 840 CALMODULIN-BINDING (POTENTIAL).
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen P., Watson D.C., Dixon G.H.;
"The hormonal control of activity of skeletal muscle phosphorylase kinase. Amino-acid sequences at the two sites of action of adenosis 3':5'-monophosphate-dependent protein kinase.";
Eur. J. Biochem. 51:79-92(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
MEDLINE=91340693; PubMed=1874721;
Harmann B., Zander N.F., Kilimann M.W.;
"Isoform diversity of phosphorylase kinase alpha and beta subunits generated by alternative RNA splicing.";
J. Biol. Chem. 266:15631-15637(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wuellrich A., Hamacher C., Schneider A., Kilimann M.W.; "The multiphosphorylation domain of the phosphorylase kinase alpha M and alpha I subunits is a hotspot of differential mRNA processing and of molecular evolution.";
                                                                                            EMBL; J03247; AAA31446.1; ALT_SEQ.
EMBL; M64656; AAC23909.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94043107; PubMed=8226841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=75130982; PubMed=164350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90201066; PubMed=2108025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE SPLICING (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=2; Synonyms=BC;
IsoId=P18688-2; Sequence=VSP_004701;
Name=3; Synonyms=Alpha';
IsoId=P18688-3; Sequence=VSP_004699, VSP_004700;
IISOId=P18688-3; Sequence=VSP_004699, VSP_004700;
IISSUE SPECIFICITY: Isoform 1 predominates in muscle, heart, brain and testis. Isoforms 1 and 2 are expressed in similar quantities in the other tissues. Isoform 3 is highly expressed in slow muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY: Glycogen metabolism.

PATHWAY: Glycogen metabolism.

SUBUNIT: POLYMER OF 16 CHAINS, FOUR EACH OF ALPHA, BETA, G
SUBUNIT: POLYMER OF 16 CHAINS, FOUR EACH OF ALPHA, BETA, G
                                                                                                                                                                                                                                                                                                                                                                                         PTM: THE PHOSPHORYLATION OF SERINE 1018 BY FKA STIMULATES DEPHOSPHORYLATION OF THE BETA SUBUNIT AND, THUS, REVERSES INITIAL STIMULATION OF PHK BY THE FASTER BETA SUBUNIT PHOSPHORYLATION THROUGH PKA THAT OCCURS IN MUSCLE IN RESPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3; Name=1; Synonyms=ABC, Alpha; IsoId=P18688-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND DELTA. ALPHA AND BETA ARE REGULATORY CATALYTIC CHAIN, AND DELTA IS CALMODULIN ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                    CHAINS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND BY CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME REGULATION: BY PHOSPHORYLATION OF VARIOUS SERINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE IN CERTAIN SUBSTRATES, INCLUDING TROPONIN I. THE ALPHA CHAIN MAY BIND CALMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PHOSPHORYLASE B KINASE CATALYZES THE PHOSPHORYLATION OF
                                                                                                                                                                                                                                                                                                                                                                           ADRENALIN
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                                                                                                                                                                                                                                                                                                                                                  TY: BELONGS TO THE PHOSPHORYLASE B KINASE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                  REVERSES THE
                                                                                                                                                                                                                                                                                                                                                                                             IN RESPONSE
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28-FEB-2003
                                                                                                                                                                                                                                                     Iorberg A., Kirchrath L., Ernst J.F., Heinisch J.J.;
"Genetic and biochemical characterization of phosphofructokinase from
the opportunistic pathogenic yeast Candida albicans.";
Eur. J. Biochem. 260:217-226(1999).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
fructose 1,6-bisphosphate.
-!- ENZYME REGULATION: Allosterically inhibited by ATP and activated
by AMP and fructose 2,6-bisphosphate.
-!- PATHWAY: Key control step of glycolysis.
-!- SUBUNIT: Heterooctamer of 4 alpha and 4 beta chains (By
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MOD RES
MOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
6-phosphofructokinase beta subunit (EC 2.7.1.11) (Phosphofructokinase
2) (Phosphohexokinase) (6PF-1-K beta subunit) (CaPFK2).
                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION STRAIN=ATCC 10231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99191702; PubMed=10091602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; mitosporic Saccharomycetales; Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans (Yeast).
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                                                                                                                                                                                                          subfamily
                                                                                                                                                                                                                  SIMILARITY: Belongs to the phosphofructokinase family. Two domains
                                                                                                                                                                                                                                                  similarity
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Similarity 37.5%;
9; Conservation
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/FTId=VSP_004699.
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InterPro; IPRO00023; Ppfruckinase.
Pfam; PF00365; PFK; 2.
PRINTS; PR00476; PHFRCTKINASE.
ProDom; PD000707; Ppfruckinase; 2.
PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.

EMBL; AJ007637; CAB38867.1; -. HSSP; P00512; 3PFK.

or send an email to license@isb-sib.ch).

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91247826; PubMed=1903915;
Froseth B.R., McKay L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M37002; AAA25202.1; -. PIR; A43746; A43746. Interpro; IPR003581; TSPC. SMART; SM00245; TSPC; 1.
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                                                                                                                Q9UHY8; Q99690; [Rel. 40, Created]
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fasciculation and elongation protein zeta 2 (Zygin II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Modecular characterization of the nisin resistance region of modecular characterization of the nisin resistance region of Lactococcus lactis subsp. lactis blovar diacetylactis DRC3.", Appl. Environ. Microbiol. 57:804-811(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibiotic resistance; Transmembrane
NCBI_TaxID=9606;
[1]
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutet
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                           Homo sapiens (Human)
                                                                                                                                                                                                              FEZ2_HUMAN
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3 946 AA; 104045 MW; AEF6167A741D8672 CRC64;
                                                                                                                                                                                                                                                                                                                                                   4 GTXXXXXSKQXEEEAVRLXXXXLKNGGXSS 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35033 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                29.8%;
26.7%;
                                                            Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
                                                                                                                                                                                                                                                                                                                                                                                             4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.5;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C8F6060250C21E48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AA.
                                                                                                                                                                                                                      320 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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              멅
                                                                                                                                                                                                                        RESULT 25
                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                           FEZ2 RAT STANDARD; PRT; 324 AA. P97578; Q9JJ35; Q9JJ36; P37578; Q9JJ35; Q9JJ36; P37578; Q9JJ35; Q9JJ36; P37578; Q9JJ35; Q9JJ36; P37579; Q9JJ36; Q9JJ36
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                   Local
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Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Pu G., Zhang Q.-H., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Pu G., Zhou J., Xu S.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Yuang G.-Y., Chen Z., Chen M.-D., Chen J.-L.; Then J.-L.; The expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length, CDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Adrenal gland;
MEDLINE=20402571; PubMed=10931946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).

-! SUBUNIT: INTERACTS WITH SYNAPTOTAGMIN.

-! SUBUNIT: INTERACTS EXPRESSED IN NONNEURAL TISSUES, SUCH-
-!- TISSUE SPECIFICITY: EXPRESSED IN NONNEURAL TISSUES, SUCH-
-!- SIMILARITY: BELONGS TO THE ZYGIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Caenorhabditis elegans gene unc-76 and its human homologs define a new gene family involved in axonal outgrowth and fasciculation."; proc. Natl. Acad. Sci. U.S.A. 94:3414-3419(1997).
-I- FUNCTION: INVOLVED IN AXONAL OUTGROWTH AND FASCICULATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 604826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:3660; FEZ2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF113124; AAF14865.1; -.
EMBL; U69140; AAB40661.1; -.
EMBL; U60061; AAC51283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloom L., Horvitz H.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE=97250552; PubMed=9096408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ugita S., von Poser C., Rosahl T.W., Hata Y., 'Zigins: a family of synaptotagmin-interacting
                                                                                                                                                                                                                                                                                                                                 Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                           ; 604826; -.
GO:0007411; P:axon guidance; TAS
GO:0007399; P:neurogenesis; TAS
                                                                                                                                                                                                                                                                                                                                                          GO:0007165; P:signal transduction; TAS
235 NKQKEHKETAKKKKKKKKKOGSSONG 258
                                                       11 SKOXEEEAVRLXXXXLKNGGXSSG 34
                                                                                                                    8
                                                                                                                                              29.8%;
Similarity 33.3%;
                                                                                                                                                                                                                                         245
320 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                         252
251
                                                                                                                                                                                                                                         36166 MW; 489CEFE0294E0015 CRC64;
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                                                                                                                                                        Score 36;
                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                             POLY-LYS
                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
                                                                                                                           Mismatches
                                                                                                                                                                                     DB 1; Length 320;
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(Zygin II) (Zygin-related

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLXA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugita S., von Poser C., Rosahl T.W., Hata Y., Suedhof T.C.; "Zigins: a family of synaptotagmin-interacting proteins related unc-76.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal sequence mutant retroviruses:evidence for increased tumorigenicity by infected rat fibroblasts."; Submitted (JAN-1999) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Q.Y., Blair D.G.; "Effective generation of viral/cell fusion transcripts by poly-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Fischer; TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 246-324 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     O87389;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-FEB-2003 (Rel. 41, Last annotation update)
Transcriptional regulator glxA.
GLXA OR R00086 OR SMC02609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions se by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents of the content of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLXA
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                                                                                                                                                                                                                  Submitted (MAR-1998)
                                                                                                                                                                                                                                                             STRAIN=1021;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                       MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         Powers E.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ZYGIN FAMILY
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                                                                                                                                                                                                                                                                                                                                                   TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 NKOKEHKETAKKKKKKKKKÓSSONG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF120110; AAF87267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SKOXEEEAVRLXXXXLKNGGXSSG 34
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 AA;
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154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTS WITH SYNAPTOTAGMIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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126
229
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                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
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Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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                                                                                   Batut J.,
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Best Local (
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000005; HTHARAC.
InterPro; IPR002818; Thid:
Pfam; PF00165; DT1_Pfp; 1.
Pfam; PF00165; HTH_ARAC; 2.
PAINTS; PR00033; HTHARAC.
SMART; SM00342; HTH_ARAC; PAMILY_1; 1.
PROSITE; PS00041; HTH_ARAC; PAMILY_2; 1.
PROSITE; PS01041; HTH_ARAC; FAMILY_2; 1.
PROSITE; PS01124; HTH_ARAC; FAMILY_2; 1.
PROSITE; PS01124; HTH_ARAC; PAMILY_2; 1.
PROSITE; PS01024; HTH_ARAC; PAMILY_2; 1.
PROSITE; PS01024; HTH_ARAC; PAMILY_2; 1.
PROSITE; PS01024; HTHARAC; PAMILY_2; 1.
PROSITE; PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF055582; AAC62219.1; -. EMBL; AL591782; CAC41473.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
103 RISRLGIRIGGISSGA 118
                                                                     20 RLXXXXLKNGGXSSGA 35
                                                                                                                                                       œ
                                                                                                                                                                                                                                                                                                               324 AA; 34959 MW;
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                                                                                                                                                       Conservative
                                                                                                                                                                                            29.8%;
                                                                                                                                                           2
                                                                                                                                                                                                                             Score 36;
                                                                                                                                                           Pred. No. 49;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   4D622F5473575D0D
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                                                                                                                                                                                                                                     DB 1; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galibert F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             symbiont
                                                                                                                                                               0
                                                                                                                                                               Gaps
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RESULT 27
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                          NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VACCC
                                                                                                                                            Virology 179:517-563(1990).
                                                                                                                                                                                                                                           Virology
                                                                                                                                                                                                                                                                             Paoletti E.;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                                           Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                           Vaccinia virus (strain Copenhagen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VP35
                                                                                                                                                                            Paolettí E.;
                                                                                                                                                                                                             COMPLETE GENOME
                                                                                                                                                            "Appendix to 'The complete DNA sequence of vaccinia virus'.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           [mmunodominant envelope protein p35 (Virion envelope protein p35).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VACCC
                                                                                                                                                                                                                                                           complete DNA sequence of vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                            TaxID=10249;
                                                                                                                                                                                                                                                                                           S.J., Johnson G.P.,
                                                                                                                                                                                        S.J., Johnson G.P.,
                                                                                                                                                                                                                                             179:247-266 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                             Perkus M.E., Davis S.W.,
                                                                                                                                                                                                                                                                                              Perkus M.E., Davis S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AA
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                                                                                                                                                                                                 Winslow J.P.
                                                                                                                                                                                                                                                                                                Winslow J.P.,
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VP35 VARY

VP35 VARY

ID VP35

AC P3305

DT 01-00

DT 01-00

DT 01-00

OC Ortho

OC Ortho

OC Virus

OC Virus

CO Virus

RR A Gashi

RA 
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Best Local :
                                                                                                                                Best
                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-India-1967 / Isolate Ind3;
MEDLINE-93190624; PubMed-8383392;
Shchelkunov S.N., Blinov V.M., Totmenin A.V., Marennikova S.S., Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytorov V.V., Gashikov P.V., Belanov E.F., Belavin P.A., Resenchuk S.M., Andzhaparidze O.G., Sandakhchiev L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P33059;
01-0CT 1993 (Rel. 27, Created)
01-0CT 1993 (Rel. 27, Last sequence update)
16-0CT 2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR004900; Pox P35.
Pfam; PF03213; Pox P35; T.
Envelope protein: Late protein.
SEQUENCE 324 AA; 37458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M35027; AAA48090.1; -. PIR; C42514; C42514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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InterPro; IPR004900; Pox_P35.
Pfam; PF03213; Pox_P35; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variola virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                               EMBL; X67119; CAA47585.1; -.
EMBL; S55844; AAB24682.1; -.
EMBL; X69198; CAA49027.1; -.
                                                                                                                                                                                                            Envelope protein; Late protein. SEQUENCE 325 AA; 37695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Res. 27:25-35(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence analysis of variola virus HindIII M, L, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunodominant envelope protein
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                                                                                                    Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALNIVDEIIKSGGLSSG
  ALNIVDEIIKSGGLSSG
                                                     AVRLXXXXLKNGGXSSG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211
     212
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                                                                                                                                Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                            EAB2FEE3CDEA6E40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cation update)
p35 (Virion envelope protein p35).
                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325
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                                                                                                                                                         DB 1; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
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                                                                                                          <u>٠</u>.
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BARRE

Q59203; 01-NOV-1997 28-FEB-2003 15-SEP-2003

(Rel. 35, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)

CPXP

BRAJA

CPXP

BRAJA

STANDARD;

PRT;

401 AA

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В
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RESULT
                                                                                                          Matches
                                                                                                                                   Query Match
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
8-amino-7-oxonomanoate synthase (EC 2.3.1.47) (AONS) (8-amino-7-keto-8-amino-pelargonic acid synthetase)
(7-keto-8-amino-pelargonic acid synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   066875;
                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000699; AAC06836.1; -. PIR; G70355; G70355. HSSP; P12998; 1BSO.
                                                                                                                                                                                     Complete proteome. BINDING 223
                                                                                                                                                                                                                                                                                              InterPro; IPR003408; Ala_synthase.
InterPro; IPR004339; Aninotransf1/2.
InterPro; IPR004723; Biop.
InterPro; IPR001917; NHtransf_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquifex aeolicus.
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                  PROSITE; ps00599; AA_TRANSFER_CLASS_2; 1.
Biotin biosynthesis; Transferase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                              Pfam; PF02490; ALA synthase; Pfam; PF00155; aminotran 1 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXONONANOATE + COA + CO(2).

COFACTOR: Pyridoxal phosphate (By similarity).

PATHWAY: Biotin biosynthesis; first step.

SIMILARITY: BELONGS TO CLASS-II OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR AQ 626
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                                                                           16 EEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetase) (L-alanine--pimelyl CoA ligase)
                                                                                                        9
                                                                                                                       Similarity
                                             EESIRV----LKEAGLGSGA
                                                                                                                                                                                                                                      TIGRO0858; bioF;
                                                                                                                                                                     373 AA;
                                                                                                          Conservative
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                                                                                                                                                                                     223
                                                                                                                                                                      42532 MW;
                                                                                                                       29.8%;
                                                                                                                                                                                                                                                                e; 1.
                                                                                                        ω
••
                                                                                                                                                                                     PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                         Score 36;
Pred. No.
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                                                                                                                                                                     536B34A5D5F84401 CRC64;
                                                                                                           Mismatches
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                                                                                                                                        DB 1;
                                                                                                                                        Length 373
                                                                                                           4.
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                                                                                                                                           Query Match
Best Local S
Matches 11
                                                                                                                                                           METAL
CONFLICT
CONFLICT
                                                                                                                                                                                                                         InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450;
PROSITE; PS00086; CYTOCHROME_P450; 1.
Cxidoreductase; Monooxygenase; Electron transport; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=USDA 110;
MEDLINE=22464998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamura Y., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tully R.E., Keister D.L.;
"Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japonicum that is expressed anaerobically and symbiotically.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytochrome P450 BJ-1 (EC 1.14.14.-) (Cytochrome P450 112). CYP112 OR BLR2144. Bradyrhizobium japponicum. Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                      PIR; I40208; I40208.
HSSP; Q00441; IOXA.
                                                                                                                                                                                                                                                                                                                                                           EMBL; U12678; AAC28889.1; -. EMBL; AP005942; BAC47409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tully R.E., van Berkum P., Lovins K.W., Keister D.L.; "Identification and sequencing of a cytochrome P450 gene cluster from Bradyrhizobium japonicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=USDA 110; PubMed=9655913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1398:243-255(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-USDA
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                                                                                                                                                                                                             complete proteome.
221
                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Environ. Microbiol. 59:4136-4142(1993).
                                12 KOXEEEAVRLXXXXLKNGGXSSGA 35
                                                                   Similarity 45.8
11; Conservative
KASEEEAVGLAAGMLVAGHESTVA 244
                                                                                                                                       350 350 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
251 L -> H (IN REF. 1 AND 2).
275 275 276 E -> Q (IN REF. 1 AND 2).
401 AA; 44473 MW; 41DF690D11FDD45A CRC64;
                                                                                   29.8%;
                                                               Score 36; DB 1; Length 401; Pred. No. 61; 1; Mismatches 12; Indels
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                                                               Gaps
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Search completed: December 23, 2003, 10:01:58 Job time : 12 secs

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Result
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Maximum DB
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Perfect score:
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          444444
44367889944444
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                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
          protein search, using sw model
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1: sp_archea:*
2: sp_bacteria
                                                                                                                                                                                                                                                                                   Match Length DB
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121
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       Minimum Match 0%
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sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_plant:*
sp_rodent:*
sp_virus:*
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sp_vertebrate:*
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sp_phage:*
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Q9CIF8
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p89451 herpes simp
Q9cif8 lactococus
Q8zews salmonella
Q8zef1 salmonella
Q8zef1 salmonella
Q8zef1 salmonella
Q8zef1 secherichia
Q8ry9 escherichia
Q9rrj0 deinococcus
Q9adj9 streptomyce

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8udb8 agro	C	16	J	31.4	
9183 scaptomyz	\vdash	ហ	4	31.4	
04317 scaptomyz	043	u	4	31.4	
9ltv4 arabido	┍	10	w	31.4	
pzu6 hepatitis	Q9PZU6	12	\vdash	Ė	38
54875 rattu	~1	11	0	Ë	œ
1729 zea	Q41729	10	653	31.8	38.5
81mq9 oryza	Q8LMQ9	10	N	Ë	œ
9kzk2 strep	Q9KZK2	16	7	Ľ	8
9cfa2 lacto	Q9CFA2	16	4		
8pu41 metha	Q8PU41	17	05	N	
814z	Q8L4Z5	10	œ	'n	
9zk11 helicobac	Q9ZK11	16	œ	ν.	
25812 helicobac	025812	16	œ		
8w2z9 oryza sati	Q8W2Z9	10	4	,	
988f6 rhizobium	Q988F6	16	œ		
31180 p	311	N	4	N	
9r733 p	9R7	N	4	N	
9r2t7 p	Q9R2T7	N	4	N	e e
9z3u2 p	923	N	4	N	
94 p	058594	17	0		
ae	707	N	4	Ņ	
Q9nkp4 leishmania	9NK	u	œ	ω	
∌	Q9KGX3	N	29	ω.	
vzk7 drosophi	Q9VZK7	σ	7		
8t919 drosophi	Q8T919	υ	J		
59 arabidops	Q9SN69	10	7		
9sd72 arabidopsi	Q9SD72	10	0		
gnx7 leishmania	Q9GNX7	υ	σ		
abidop	Q9LHL3	10	ທ		
u184 leis	Q9U184	υī	J	ω •	
96631 bacillu	P96631		N	ω	40
8pli3 xanth	Q8PLI3	16	S	ω.	
6 d 8	286480		91		

ALIGNMENTS

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STRANN=HG52; PubMed=2161906;
MEDLINE=90278430; PubMed=2161906;
Everett R., Fenwick M.;
"Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 en a truncated UL41 product.";
a truncated UL41 product.";
J. Gen. Virol. 71:1387-1390(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                             P89451 PRELIMINARY;
P89451;
01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                              MEDLINE-87111457; PubMed=3027242; MCGeoch D.J., Moss H.W., MCNab D., Frame M.C.; Together in the short "DNA sequence and genetic content of the HindIII 1 region in the short unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary
SEQUENCE FROM N.A.
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                               Herpes simplex virus (type 2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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                                                                                                                                                                                         comparisons.";
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10310;
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Last sequence update)
Last annotation updat
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A Weissenbach J., Ehrlich S.D., Sorokin A.;

T "The complete genome sequence of the lactic acid bacterium Latting It.403.";

I Genome Res. 11:731-753(2001).

EMBL; AE006277; AAR0450S.1;

R EMBL; AE006207; AAR0450S.1;

R InterPro; IPR006204; GHMP kinase.

R InterPro; IPR006206; Mev_galkinase.

Pfam; PF00288; GHMP kinases; 1.

R PFINTS; PR00959; MEVGALKINASE.

W Kinase; Complete protecme.

SEQUENCE 310 AA; 34334 MW; E85A2C962C943BDA CRC64;
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Best Local
                                                                                                           Matches
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Q9CIF8;
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
Meyalonate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Pfam; PF01366; PRTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92356101; PubMed=1322965;
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MEDLINE=92113549; PubMed=1662697;
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285
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                                                                                                           Similarity 7; Conserv
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                                                    QXEEEAVRLXXXXLKNGGXSS 33
ENEKDAIRISQRLLKNGAKNT 305
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41.7%;
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                                                                                                        7; Mismatches
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Last annotation updat
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Pred. No. 20;
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Pred. No. 23;
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RESULT 3

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RESULT 4
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Pfam; PF02878; PGM_PMM_I; 1.
Pfam; PF02879; PGM_PMM_II; 1.
Pfam; PF02880; PGM_PMM_III; 1.
TIGRFAMS; TIGR01132; Pgm; 1.
PROSITE; PS00710; PGM_PMM; 1.
                                                                                                                                                                                                                                                                             Q8Z8F1;
Q8Z8F1;
01-MAR-2002 (TIEMBLICEL 2
01-MAR-2002 (TIEMBLICEL 2
01-MAR-2003 (TIEMBLICEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8ZQW9 PRELIMINARY; PRT; 546 AA.
Q8ZQW9;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Phosphoglucomutase (EC 5.4.2.2).
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T., Holtoyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                               STY0736.
Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005852; Pglucomut_A.
InterPro; IPR005844; PG PMM_ABAII.
InterPro; IPR005845; PG_PMM_ABAII.
InterPro; IPR005844; PG_PMM_ABAIII.
InterPro; IPR005844; PG_PMM_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Di F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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InterPro; IPR005842; P9Iucomut A.
InterPro; IPR005842; P9Iucomut A.
InterPro; IPR005844; PG_PMM_ABAII.
InterPro; IPR005844; PG_PMM_ABAIII.
InterPro; IPR005846; PG_PMM_ABAIII.
InterPro; IPR005846; PG_PMM_CC.
Pfam; PF00400; PGM_PMM; 1.
Pfam; PF00400; PGM_PMM; 1.
Pfam; PF02879; PGM_PMM_I; 1.
Pfam; PF02879; PGM_PMM_II; 1.
TIGREAM9; TIGR01372; PGM_PMM_II; 1.
TIGREAM9; TIGR01372; PGM_PMM_II; 1.
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STRAIN=0157:H7 / EDL933 / ATCC 700927;

STRAIN=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                    Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
                                                                                                                             InterPro;
InterPro;
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STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-2115621; PubMed=11258796;
                                                                                                                                                                                   EMBL; AE005247; AAG55011.1; -. EMBL; AP002552; BAB34142.1; -.
                                                                   InterPro;
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PGM OR Z0837 OR ECS0719.
Escherichia coli 0157:H7.
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01-MAR-2002 (TrEMBLrel. 20, Last seg
01-MAR-2003 (TrEMBLrel. 23, Last ann
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o; IPR005841; PG/PMM_mutase.
j; IPR005852; Pglucomut A.
pr005844; PG_PMM_ABAII.
p; IPR005845; PG_PMM_ABAIII.
p; IPR005846; PG_PMM_ABAIII.
p; IPR005843; PG_PMM_C.
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52.9%;
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Pfam; PF02878; PGM_PMM_I; 1.
Pfam; PF028879; PGM_PMM_II; 1.
Pfam; PF02880; PGM_PMM_III; 1.
TIGREPAMS; TIGR01132; Pgm; 1.
PR0SITE; PS00710; PGM_PMM; 1.
MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F.,
                                                                                               Deinococcus radiodurans,
Bacteria; Deinococcus-Thermus;
                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
Hypothetical protein DR2500.
                            STRAIN=R1
                                            SEQUENCE FROM N.A.
                                                                                   Deinococcaceae; Deinococcus
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBFJV9 PRELIMINARY; PRT; 563 AA. QBFJV9; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Phosphoglucomutase (EC 5.4.2.2).
                                                                     NCBI_TaxID=1299;
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EMBL; AE016757; AAN79248.1; -.
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MEDLINE=22388234; PubMed=12471157;
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NCBI_TaxID=217992;
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 Hickey E.K.,
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                                                                                                                                                                                                                                                                      coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                  Hypothetical SEQUENCE 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
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                                                                                                                                                         EMBL; AL939122; CAD30959.1; -.
InterPro; IPRO02125; dCMP/Cyt deam.
Ffam; PP00383; dCMP cyt deam; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 167 AA; 18334 MW; 3D2044BAI1F6E9B1 CRC64;
                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces
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                                                                             Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
           EEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEAVRLXXXXLKNGGXSSG
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.9%; Score 41; 42.1%; Pred. No.
                                                                      33.9%; Score 41; DB
35.0%; Pred. No. 15;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 AA
                                                                                                                 DB 16; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                     Q9UYT6; PRELIMINARY; PRT; 402 AA.
Q9UYT6; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      092527
                                                                                  structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL, AJ248287; CAB50326.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO00052; Pitvir_coat.
Pfam; PF00286; virus P-coat; 1.
PRINTS; PR00232; POTXCRICOAT:
ProDom; PD000603; Pitvir_coat; 1.
PROSITE; PS00418; POTEX_CARLAVIRUS_COAT; 1.
              InterPro; IPR001453; MoCF_biosynth
InterPro; IPR005111; MoeA_C.
InterPro; IPR005110; MoeA_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE POTEXVIRUSES COAT PROTEIN FAMILY EMBL; AJ010697; CAA09306.1; -. EMBL; X52627; CAA36854.1; -.
                                                                                                                                                                            Heilig
                                                                                                                                                                                               STRAIN=GE5 / Orsay;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                   Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                        PAB1436
                                                                                                                                                                                                                                                                                                                                                                         Molybdenum cofactor biosynthesis protein (MOEA-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91324119; PubMed=1713905; Meehan B.M., Mills P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coat protein (Capsid protein).
Carnation latent virus (CLV).
                                                                                                                                             Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                              NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Leaves of Dianthus barbatus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meehan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=12164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of the 3'-terminal region of carnation latent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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PF00994; MoCF_biosynth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KLKEFNSONLTAGELKNGGFESG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 KOXEEEAVRLXXXXLKNGGXSSG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 AA; 33890 MW; 4456EBB53E174298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TremBLrel. 08, Created)
(TremBLrel. 08, Last sequence update)
(TremBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 306;
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RESULT 12
Q8C7V2
                     ARRAR ROCCOSTORIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
STRAIN=C57BL/6J;
MEDLINE=22354683; PubMed=12466851;
The FANTOW Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annot
                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ectodermal-neural cortex 1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01344; Kelch; 5.

MART; SM00225; BTB; 1.

SMART; SM00612; Kelch; 6.

PROSITE; PS50097; BTB; 1.

PROSITE; PS00639; THIOL PROTEASE HIS; 1.

PROSITE; PS00639; THIOL PROTEASE HIS; 1.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feng Z., Zhang B., Peng X., Yuan J., Qiang B.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY049781; AAL15438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pfam; PF03453; MoeA_N; 1.
ProDom; PD002460; MoCF_biosynth; 1.
TIGRFAMs; TIGR00177; molyb_syn; 1.
                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000210; BTB_POZ.
InterPro; IPR006652; Kelch_rep_InterPro; IPR000169; SHprot_ace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ectodermal-neural cortex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69T96D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 SKEIVEEAIRCKLKILONDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SKOXEEEAVRLXXXXLKNGG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00651; BTB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
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9; Conserv
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45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 589;
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      on functional annotation
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RESULT 13
Q8BRG4
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Matches
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Q8BRG4;
O1-MAR-2003 (TrEMBLrel. 23, C
O1-MAR-2003 (TrEMBLrel. 23, L
O1-MAR-2003 (TrEMBLrel. 23, L
Ectodermal-neural cortex 1.
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktarogiu L., Beasley E.M.,
                                                                                                                                                                                                             CG5406 protein.
SIF OR CG5256 OR CG5406.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Drosophila.
                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                      STRAIN-Berkeley;
                                                                                                                                                                                                Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Q9VRN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK044906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK049187; BAC33597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 SKEIVEEAIRCKLKILONDG 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SKOXEEEAVRLXXXXLKNGG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC32136.1;
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Pred. No. 60;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53C00CA49EA86B85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Kecchum K.A.,
RA Harris N.L., Harvey D., Heimann T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kecchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mobhrefi A.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syier E., Syradling A.C., Stapleton M., Skupskin M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y. Wassarman D.A., Weinsteck G.M., Wang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J., Smith H.O.,
RN [71]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Banzon J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson K., Dorsett V., Doup L.E., Doyle C., Dreenek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
T. "Sequencing of Drosophila melanogaster genome.";
T. "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smithiak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
                 FlyBase; FBgn0019652; sif.
InterPro; IPR001331; GDS_CDC24
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Celniker S.E., Adams M.D.,
                                                                 -i-SIMILARITY: CONTAINS 2 P. EMBL, AE003565; AAF50756.3; HSSP, P08567; IPLS.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               Adams M.D., Celniker
Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                       EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                     Rubin G.M.,
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RESULT 15
Q8MT93
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Matches
                                                       Query Match
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Best Local Similarity
                                                                                                                          Pfam; PF00169; PH; 2.

Pfam; PF00821; RhOGEF; 1.

Pfam; PF00821; RhOGEF; 1.

SMART; SM00228; PDZ; 1.

SMART; SM00233; PH; 2.

SMART; SM00335; RBD; 1.

SMART; SM00335; RBD; 1.

SMART; SM00325; RhoGEF; 1.

PROSITE; PS000741; DH 1; 1.

PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02196; RBD; 1.

Pfam; PF02196; RhoGEF; 1.

Pfam; PF00621; RhoGEF; 1.

SMART; SM00223; PH; 2.

SMART; SM00233; PH; 2.

SMART; SM00325; RBD; 1.

SMART; SM00325; RBD; 1.

SMART; SM00325; RBD; 1.

PROSITE; PS00741; DH_1; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS50103; PH DOMAIN; 1.

SEQUENCE 2052 AA; 228954 MW; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Par Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GH10341p.
SIF OR CG5256 OR CG5406.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0019652; sif.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY118305; AAM48334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO
Pfam; PF00169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003116; RBD.
InterPro; IPR000219; RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR000219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR001849; PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1769 ROIIRESVRNMSIPMKNFGGSSGS 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 KOXEEEAVRLXXXXLKNGGXSSGA 35
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JUN-2002) to the
                                                                                                                 2061 AA;
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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41.7%;
                           41.7%;
                                                       33.9%;
                                                                                                              229930 MW; 5A1621A34E5149DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                           Score 41; DB 5; Length 2061; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 5;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAINS
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8C5591ED80E5CC32 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Park S.,
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1778 12

KOXEEEAVRLXXXXLKNGGXSSGA 35

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RA Adams M.D. (Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. (Calniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. (Calniker S.E., Holt R.A., Sabburner M., Henderson S.N., RA Bananatides P.G., Scherer S.E., Holt R.A., Sabburner M., Henderson S.N., RA Bananatides P.G., Scherer S.E., Richards S. Ababburner M., Henderson S.N., RA Banton R.C., Mortman J.R., Xandell M.D., Zhang Q., Chen L.X., RA Burtin R.G., Mortman J.R., Xandell M.D., Zhang Q., Chen L.X., RA Burandon R.C., Mortman J.R., Xandell M.D., Zhang Q., Chen L.X., RA Burandon R.C., Moltos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxerdale J., Bayrakarargul L., Beasley E.M., RA Beeson K.Y., Benos P.V., Bemman B.P., Bhandari D., Bolshakov S., RA Borrkova D., Botchan M.R., Bouck J., Broktein P., Brottier P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Doubles R.A., Bouck J., Boltier R.A., Deng Z., Mays A.D., Dew I., Dietz S.M., Durbin K.J., Evangelista C.G., Ferraz C., Ferriera S., Flesschmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M., Harris M., Glassear K., Ra Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., RA Harris N.L., Matrei B., Mothrosh T.G., McLeod M.P., Moshrefi A., Kitchum K.A., Katchum S., J., Ling Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Y., Li J., Ling Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li M., Moshrefi A., Mount S.M., Welson K.A., Nixon K., Nuzskern D.R., Nelson D.L., Ratit C., Kratt C., Kravitz S., Kulp D., Liai Z., RA Mount S.M., Welson K.A., Nixon K., Nuzskern D.R., Pacleb J.M., Nelson D.L., Welson D.C., Scheeler F., Spen H., Rub J., Ling Y., Lin X., Ra Mary M. H., Welson K.A., Nixon K., Nuzskern D.
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Barazon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferrierz S., Frise E. Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Paragas V., Park S., Patel S., Pfeiffer B.,
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG5406 protein.
SIF OR CG5256 OR CG5406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9VRN7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VRN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQIIRESVRNMSIPMKNFGGSSGS 1801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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RRR COCOG E DITION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02196; RBD; 1.
Pfam; PF02196; RbDGEF; 1.
SMART; SM00228; PDZ; 1.
SMART; SM00233; PH; 2.
SMART; SM00455; RBD; 1.
SMART; SM00455; RBD; 1.
SMART; SM00456; WHI; 1.
SMART; SM00461; WHI; 1.
PR0SITE; PS00741; DH 1; 1.
PR0SITE; PS50010; PDZ; 1.
PROSITE; PS50003; PH_DOMAIN;
PROSITE; PS50003; PH_DOMAIN;
                                                                                                                                                                                                                                                                   QBP9Q5;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation updat
Filamentous hemaagglutinin.
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"Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: CONTAINS 2 PH DOMAINS EMBL; AE003565; AAF50755.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00169; PH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0019652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         issp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1789 RÓIIRESVRNMSIPMKNFGGSSGS 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 KOXEEEAVRLXXXXLKNGGXSSGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2072 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker S.E.,
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A; 231130 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%;
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the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 5;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3CAFE543F72DD331 CRC64;
                                                                                                                                                                                                                                                                                                                                                      2918 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=ATCC 33913 / NCPPB 528

SEQUENCE FROM N.A. NCBI_TaxID=340; Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

0

Kanthomonadaceae; Xanthomonas.

FHAB OR XCC1794.

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В
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RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vicorello C.B., Van Slys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Nachado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Marrins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Trindade dos Santos M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Schubal J.C., Kitajima J.P.;
RA Setubal J.C., Kitajima J.P.;
RI "Comparison of the genomes of two Xanthomonas pathogens with differing
RT "Nett specificities";
RI Nature 417.459-463(2002).
RM Comblete proteome.
RESULT 18
                                                                                       RC STRAIN—306 / ATCC 13902 / XV 101;

RC MEDLINE=22022145, pubMed=12024217;

RA MEDLINE=22022145, pubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Perreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.E., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.E., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Atsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Findade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RI "Comparison of the genomes of two Xanthomonas pathogens with differing

RT Note specificities ";

RMBL, AE011814, AAM366771;

- BMBL, AE011814, AAM366771;

- BMBL, AE011814, AAM366771;

- BRBL, AE011814, AAM366771;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01.0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Filamentous haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
Complete proteome SEQUENCE 4753 A
                                                 Pfam; PF01155; HypA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8PLI3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282113
                                                                        InterPro; IPR000688; HypA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2453 EQSVRLNVQSLSNAGGQIGA 2472
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEAVRLXXXXLKNGGXSSGA 35
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45.0%;
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471484 MW;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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ABC4B22EB09DBFE9 CRC64;
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RA Azevedo V., Bortero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier I., Parans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier I., Raman A., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itya M., Jones L.,
RA Hilbert H., Holsappel S., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Laber J., Lazarevic V.,
RA Kotayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Nonne D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Reymolds S.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler E., Vasnane K., Vasnmoto K., Yata K.,
RA Vishida K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.,
RT The complete genome sequence of the gram-positive bacterium Bacillus
RT The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P96631
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01-MAY-1997 (TrEMBLrel. 03,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2002 (TrEMBLrel. 20,
                               Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBU databases.
EMBL; AB001488; BAA19320.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beloin C., Ayora S., Exley R., Hirschbein L., Ogasawara N.,
Kasahara Y., Alonso J.C., Le Hegarat F.;
"Characterization of an lrp-like (lrpC) gene from Bacillus subtilis.";
Mol. Gen. Genet. 256:63-71(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98000887;
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                                                                                                                STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2452
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                                                                                                                                                                          390:249-256(1997).
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                                                                                                                                   FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9341680;
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Pred. No. 5.8e+02;
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interPro;

Pro; IPR001387; HTH_3: PF01381; HTH_3; 1.

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RESULT 21
Q9LHL3
    RAGE OOC OOK STANKER OOC OOK STANKER OOK S
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Q9U184
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LHL3 PRELIMINARY; PRT; 455 AA.
Q9LHL3;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-2000
01-DEC-2001
STRAIN=Columbia,
                                    SEQUENCE FROM N.A.
                                                                                                                 Submitted
                                                                                                                                             STRAIN=Columbia;
Kaneko T., Kato T.,
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-binding protein-like.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
EMBL; AL133468; CAB63133.1; -.
Hypothetical protein.
SEQUENCE 374 AA; 41675 MW; AA38847D8E433937 CRC64;
                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wedler H., Hilbert H., Duesterhoeft A., Ivens A.C., Murj
Quail M., Rajandream M.A., Barrell B.G.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
IVens A.C., Lewis S.M., Bagherzadeh A.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Friedlin;
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L3238.06.
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8; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOXEEEAVRLXXXXLKNGGXSSG 34
                                                                                                                 (MAY-2000)
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.1%; Si ilarity 47.1%; Pi Conservative 2;
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                                                                                                                                                 Sato
                                                                                                 3ato S., Nakamura Y., Asamizu E., Tabata
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.1%; Score 40; 39.1%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 23
Q9SD72
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Q9GNX7
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Best Local (
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QSD72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A physical map of the Leishmania major Genome Res. 8:135-145(1998).
EMBL, AL358652; CAC18989.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 567 AA; 60584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98146435; PubMed=9477341; Ivens A.C., Lewis S.M., Bagherzad Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Friedlin;
Bothe G., Pohl T., Ivens A.C., Quail M.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GNX7
Q9GNX7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical 60.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00076; rrm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom
InterPro; IPR005504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002041; BAB02607.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 EEEAVRLXXXXLKNGGXSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 KQXEEEAVRLXXXXLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.1%;
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41.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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Pred. No.

 Mismatches

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Pred. No. 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 567
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Q9SN69
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Best Local
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Submitted (JAN-1999) to the EMBL/GenBank/DI
Submitted (JAN-1999) to the EMBL/GenBank/DI
EMBL; AL133292; CAB61947.1;
InterPro; IPR002772; Glyco_hydro_3C.
InterPro; IPR001764; Glyco_hydro_3N.
Pfam; PF00933; Glyco_hydro_3; 1.
Pfam; PF01915; Glyco_hydro_3 C; 1.
PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
                                             EMBL; AL021768; CAB40378.1; -.
EMBL; AL161551; CAB78963.1; -.
InterPro; IPR000504; RNA_rec_mot
Pfam; PP00076; rrm; 3.
EMART; SM00350; RRM; 3.
                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G
                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Vitale D., Liguori R., Argiriou A.,
Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
Hypothetical 86.7 kDa protein.
F2447.162 OR A74G19610.
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Choisne N., Robert C., Brottier P., Wincker P., Cattolic Choisne N., Robert C., Brottier P., Wincker P., Cattolic Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., L Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9SN69
                           PROSITE;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                     Vitale D.,
Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9SN69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376
                     SM00360; RRM; 3.
E; PS50102; RRM; 3.
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                                                                                                                                                                                                                                                                                                                                     Liguori R.,
Mayer K.F.X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   609 AA;
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protein
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38.5%;
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Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                             V., Mewes H.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                databases
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RESULT
Q8T919
ID Q8
   RESULT 26
Q9VZK7
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Best Local
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Best Local
       MEDLINE-2019606; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Man K.H., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow B.M., Bayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow B.M., Bayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow B.M., Bayani A., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                               Q9VZK7
Q9VZK7;
                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Bukaryota; Brdopterygota; Diptera; Brachycera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frisc George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Pat Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8T919;
Q8T919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                 STRAIN=Berkeley;
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                CG14982
                                                                                                                                                                                                                                                                                            CG14982 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; A7075166; AAL68036.1; -. FlyBase; FEBGN0035477, CG14982. SEQUENCE 773 AA; 84788 MW; 080468E1D601FCDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002
01-JUN-2002
                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEEAV--RLXXXXLKNGGXSSGA 35
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                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.1%;
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Baxendale J., Bayraktaroglu L.,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                               Created)
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Pred. No. 1.2e+02;
"""matches 7;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
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                                                                                                                                                                                                                                           Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 773;
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Beasley
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RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Doddson K., Doysett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

RA Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genn P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mcivalov G., Milshina N.V., Mobarry C., Morris J., Moshirefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshirefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Williams S.M., Woodsge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wing R.A., Zhong W., Shong W., Zhan M., Zhang G., Zhon Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhon Q., Zheng L.,
RA Yellan S.M., Woodsge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
The genome sequence of Drosophila melanogaster.",
RN M. Science 287:2185-2195(2000)
     Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                             Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE003479; AAF47814.2; -. FlyBase; FBB90003477; CG14882. SEQUENCE 773 AA; 84832 MW; E1D9789DE2AD912C CRC64;
                                                                                                                                                                                                                                                                                     Adams M.D., Celniker
Submitted (MAR-2000)
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                           Similarity
                                                                                                                                                                                                                                                                                                              Celniker
                           33.1%; Score 40; 43.5%; Pred. No.
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to the
                                                                                                                                                                                                                                                                                  Gibbs R.A., Rubin (
e EMBL/GenBank/DDBJ
                                                                                                  E1D9789DE2AD912C CRC64;
     Mismatches
                           1.2e+02;
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                                                    DB 5;
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Q9KGX3
ID Q9KGX
AC Q9KGX
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NKP4;
                                                                                                                                                                                                                                    Worthey E.A., Siek E., Hixson G., Kiser P., Rickel E., H Cawthra J., Sunkin S., Stuart K.D., Myler P.J.; "Direct Submission.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005930; AAF39730.1;
EMBL; AC125735; AAM69050.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KGX3
Q9KGX3;
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Friedlin;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Friedlin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmania major.
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BQ14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Adjacent sequence of Mycoplasma hyopneumoniae ABC transporter Pr1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verdin E., Saillard C.;
1352 QRSHEKVRLSAAGVKNGSSAA 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                960
                                                 13 OXEEEAVRLXXXXLKNGGXSS 33
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                                                                                                                                  Similarity
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                                                                                                                                                                                                                2382 AA;
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                                                                                                        Conservative
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ilarity 39.1%;
Conservative
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                                                                                                                               33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                250422 MW;
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Pred. No. 2.2e.
3; Mismatches
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Last annotation updat
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Pred. No. 4.2e+02;
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                                                                                                     Mismatches
                                                                                                                                                                                                          838E575E5927E737 CRC64;
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                                                                                                                                                   Length 2382;
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RESULT 29
P70746
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058594
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Best Local S
Matches 9
                      DNA Res. 5:55-76(1998).

EMBL; AP000003; BAA29958.1; -.

HSSP; P29095; IAIS.

InterPro; IPR006670; Cyclin.

InterPro; IPR006812; TFIIB_euk.

Pfam; PF00382; transcript_fac2; 2.

PRINTS; PR00685; TIFACTORIIB.

SMAAT; SM00385; CYCLIN; 2.

PROSITE; PS00782; TFIIB; 1.
                                                                                                                                                                                                                                                   MEDLINE=98344137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfiku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             058594;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 23, Last annotation update)
208AA long hypothetical transcription initiation factor IIB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003097; FAD_binding.
InterPro; IPR001226; Flavodoxin.
Pfam; PF00667; FAD_binding_1; 1.
Pfam; PF00258; flavodoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TrEMBLrel 02, Created)
01-FEB-1997 (TrEMBLrel 02, Last sequence update)
01-FEB-1997 (TrEMBLrel 23, Last annotation update)
01-MAR-2003 (TrEMBLrel 23, Last annotation update)
Cyteine biosynthesis protein CysJ (Fragment).
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nes 9; Conserv
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   tactor;
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15314 MW;
Complete proteome
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Search completed: December 23, 2003, 10:03:49
Job time : 31.5 secs
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                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
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                                                38
                                                                      12 KOXEEEAVRLXXXXLKNG 29
                                               KHVEREAVRIYRKLIKSG 55
                                                                                                                                                208 AA; 23878 MW;
                                                                                               Conservative
                                                                                                          32.28;
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                                                                                                            Score 39; DB
Pred. No. 46;
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Post-processing: Minimum Match 0%
Maximum Match 10
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Maximum DB seq length: 200000000
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Perfect score:
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A Geneseq_19Jun03:*

| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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(without alignments)
173.947 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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70.5	70.5	70.5	71.5	71.5	71.5	71.5	71.5	79	Score	
62.9	62.9	62.9	63.8	63.8	63.8	63.8	63.8	70.5	Query Match	
36	36	36	39	39	37	37	37	38	% Query Match Length DB	
21	21	20	22	21	22	22	20	21	DB	
AAB53029	AAB11263	AAY17606	AAE08383	AAB11313	AAB64363	AAE08527	AAY17618	AAB52839	ID	SUMMARIES
Extendin agonist c	exendin agonist pe	agonist	agonist				Exendin agonist pe	Extendin agonist p	Description	

09.3 02.1 36 20 MAIL/603	60 5 62 1 36 20 PAV17605	69.5 62.1 36 20 AAY17619 E	69.5 62.1 36 20 AAY24837	69.5 62.1 36 20 AAY24856	6 69.5 62.1 36 20 AAY31533	69.5 62.1 35 22 AAB64353	4 69.5 62.1 35 22 AAB64249	3 69.5 62.1 35 22 AAE08517	69.5 62.1 35 22 AAE08413	1 69.5 62.1 35 21 AAY94186	69.5 62.1 35 21 AAY94074 Am:	9 69.5 62.1 35 21 AAB53031 Ext	69.5 62.1 35 21 AAB52920 Ext	69.5 62.1 35 21 AAB11265 exe	69.5 62.1 35 21 AAB11161	5 69.5 62.1 35 20 AAY17608	69.5 62.1 35 20 AAY24839	69.5 62.1 35 20 AAY31535	70.5 62.9 39 22 AAB64219	70.5 62.9 39 22 AAE08381	0 70.5 62.9 39 22 AAE08380	70.5 62.9 39 22 AAE08379	8 70.5 62.9 39 21 AAY94043	70.5 62.9 39 21 AAY94040 Ami	6 70.5 62.9 39 21 AAY94039	5 70.5 62.9 39 21 AAB11311	4 70.5 62.9 37 22 AAB64279	3 70.5 62.9 37 22 AAB64264	70.5 62.9 37 22 AAB64263	1 70.5 62.9 37 22 AAE08443	70.5 62.9 37 22 AAE08428	70.5 62.9 37 22 AAE08427	70.5 62.9 37 21 AAY94196	.5 62.9 37 21 AAB53041	70.5 62.9 37 21 AAB11275 exe	70.5 62.9 37 20 AAY24854 Exe	70.5 62.9 37 20 AAY24853 Exe	70.5 62.9 37 20 AAY24869	70.5 62.9 36 22 AAB64351	70.5 62.9 36 22 AAE08515	70.5 62.5 56 21 AMISTICS	10 F F C C C C C C C C C C C C C C C C C	מוניסעני וני אני מי
exendin agonisc pe	1	in agonist p	S	in agoni	in agoni	in agonist,	5	in agonist	Exendin agonist pe	acid se	no acid seque	endin agonist	n agonist	agonist	agonist	Exendin agonist pe	agonist	agonist	agonist,	agonist p	agonist	agon	id se	no acid se	sequen	٠,	mist,	mist,	mis	nist	onist	ĕ	9	xtendin agonist	ndin agon:	xendin agonist p	in agonist	O.	in agonist,	in agonist p	South Conde	Talla Section	שליום פו

ALIGNMENTS

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RESULT 1
AAB52839
ID AAB5
Young A,
                                                                                 09-NOV-2000.
                                                                                                                    Heloderma sp.
                                                                                                                                      Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia; insulin-resistance syndrome; food intake.
                                                                                                                                                                                    28-FEB-2001 (first entry)
                                                                                                                                                                                                        AAB52839;
                                            30-APR-1999;
                                                             28-APR-2000; 2000WO-US11814.
                                                                                                  WO200066629-A1.
                                                                                                                                                                 Extendin agonist peptide #9.
                                                                                                                                                                                                                          AAB52839 standard; Peptide; 38
                          (AMYL-) AMYLIN PHARM INC.
        Prickett K;
                                            9908-0132018
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RESULT 2
AAY17618
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                             endogenous to Arizona and Northern Mexico. The peptide agonists are used to treat diabetes mellitus (types I or II), hyperglycaemia or hypoglycaemia. They can also be used for in vitro and in vivo studies on exendins and their agonists. They regulate gastric motility and slow gastric emptying (resulting in lower post-prandial glucose levels).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to extendins and their agonists which have been modified with molecular weight increasing agents such as polyethylene glycol (PEG). These can be used in the treatment of diabetes, obesity, impaired glucose tolerance, postprandial dumping syndrome, postprandial hyperglycaemia, eating disorders, insulin resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity -
                                                                                                               AAY17535 to AAY17624 represent exendin peptide agonists. Exendins peptides that are found in the venom of the Gila-monster, a lizard
                                                                                                                                                                                                              Peptide agonists of exendin - delay stomach emptying, for treating
                                                                                                                                                                                                                                                                                 Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin agonist peptide #84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 52-53; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-672834/65.
                                                                                                                                                                Claim 28; Fig 4; 144pp; English
                                                                                                                                                                                                                                               WPI; 1999-347456/29.
                                                                                                                                                                                                                                                                                                                                                1.4-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9925728-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY17618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17618 standard; peptide;
                                                                                                                                                                                                                                                                                                                 (AMYL-) AMYLIN PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                and hypo- or hyper-glycaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTXXXXXSKQXEEEAVRLXXXXLXGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 AA;
   37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                 Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                97US-0066029
                                                                                                                                                                                                                                                                                                                                                                                98WO-US24273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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100.0%; Pred. No.
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Query Match

63.8%;

Score 71.5;

DB 20;

Length 37;

AAB64363 ID AAB

AAB64363 standard;

peptide;

37

RESULT 4

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                                                                                                                                          Best
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                                                       Matches
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                   The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                            Sequence
                                                                                                                                                                                                                                                                       Example 178; Page 143; 161pp; English.
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200151078-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diuretic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin agonist; antilipemic; cardiant; triglyceride; inotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exendin agonist peptide #172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE08527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE08527 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                   triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                 Use of exendin and exendin agonist compounds for modulating
                                                                                                                                                                                                                                                                                                                                                                         Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                                                        (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-2000; 2000US-0175365
                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-2001; 2001WO-US00719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                  Local
                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
4 GTFTSALSKOMEEEAVRLFIEWLKNGGASSGA 35
                          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GTFTSALSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coronary heart disease; dyslipidaemia
                                                                                                              37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-methyl alanine; C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.4%;
                                                                 59.48;
                                                      0,
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                                                                  Score 71.5; DB 22;
Pred. No. 2.1e-06;
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                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                Length 37;
                                                      Indels
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(first entry)

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infections. GDM results in an elevated rate of foetal abnormalities such as neural tube defects, and is associated with an increased risk of neonatal morbidites such as hypoglycaemia, hypocalcaemia, of the GC neonatal morbidites such as hypoglycaemia, hypocalcaemia, and subsequent childhood and adolescent obesity. Exendin-4 are peptides from the salivary secretions of the Gila monster (exendin-4) are peptides from the salivary secretions of the Gila monster (exendin-4) and have similar considerable family, particularly GLP-1, and have similar insulinotropic effects. Unlike the compounds used to treat type 2 diabetes, which are contraindicated for GDM, exendins and exendin agonists do not cross the placenta and thus do not cause severe prolonged hypoglycaemia in the newborn. They have a potent and prolonged effect on blood glucose, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The based upon the sequence of exendin agonist of the invention which is
                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an exendin agonist (AAB64185-B64368) for treating gestational diabetes mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished ability to increase insulin secretion. In contrast, in a normal pregnancy, both insulin resistance and insulin secretion increase. GDM pregnancy both insulin resistance and insulin secretion increase. GDM pregnancies are associated with complications in both the mother and the foetus. Women with GDM have increased rates of Caesarian delivery, hypertensive disorders such as pre-eclampsia, and urinary tract
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the use of an exendin (AAB64181-B64182) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 178; Page 119; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of exendins or exendin agonists for lowering or reducing glucose levels and treating gestational diabetes mellitus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exendin agonist, SEQ ID NO:183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  especially in a human -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200073331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heloderma suspectum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB64363;
                                                                                                               Local
                                                                                         19;
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMYLIN PHARM INC
                                      GTXXXXXKQXEEEAVRLXXXXL-XGGXSSGA 34
GTFTSALSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prickett KS
                                                                                                                                                                              37 AA;
                                                                                                                                                                                                                          the sequence of exendin-4.
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0323867
                                                                                                        63.8%;
                                                                                       0
                                                                                                        Score 71.5; DB 22
Pred. No. 2.1e-06;
                                                                                    Mismatches
                                                                                                                              DB 22;
                                                                                                                              Length
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a subject,
                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                        AAE08383;
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RESULT 5 AAB11313

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Modified-site
                                                            key
Modified-site
                                                                                                                                                            Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                            Exendin agonist peptide #30.
                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                       AAE08383 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or reducing food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 44; Figure 15; 281pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-514584/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JAN-2000; 2000US-0116380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200041546-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasma glucose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exendin agonist peptide SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L'Italien JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0116380
/note= "N-Methyl-alanine"
                                        /note= "N-Methyl-alanine"
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastric emptying; food intake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.8%;
59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kolterman O;
                                                                                                                                                                                                                                                                                                                                                         39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71.5; DB 21
Pred. No. 2.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
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Best Local S
Matches 19
                                                                                                                                                   Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin. Note: The present sequence is not shown in the specification but is derived from SEQ ID NO:3 shown in page 17 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have innotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride
            14-NOV-1997;
                                    13-NOV-1998;
                                                               27-MAY-1999
                                                                                        W09925728-A1
                                                                                                                 Heloderma
                                                                                                                                                                                                         Exendin agonist peptide #72
                                                                                                                                                                                                                                    09-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2000; 2000US-0175365
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                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                      AAY17606 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 30; Page -; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of exendin and exendin agonist compounds for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kolterman OG,
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                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                         GTFTSDLSKQLEEEAVRLFIEFLKNGGASSGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                    (first entry)
            97US-0066029
                                    98WO-US24273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-Methyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-Methyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                        59.4%;
                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                         71.5;
No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                           12;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
      This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17535 to AAY17624 represent exendin peptide agonists. Exendins are peptides that are found in the venom of the Gila-monster, a lizard endogenous to Arizona and Northern Mexico. The peptide agonists are used to treat diabetes mellitus (types I or II), hyperglycaemia or hypoglycaemia. They can also be used for in vitro and in vivo studies on exendins and their agonists. They regulate gastric motility and slow gastric emptying (resulting in lower post-prandial glucose levels).
                                                                                                                                   Example 180; Page 229; 281pp; English.
                                                                                                                                                                                 New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat
                                                                                                                                                                                                                                  WPI; 2000-514584/46.
                                                                                                                                                                                                                                                                                                                                                          10-JAN-2000; 2000US-0116380
                                                                                                                                                                                                                                                                                                                                                                                                                           WO200041546-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasma glucose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exendin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11263 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                               (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                             14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                            20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB11263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 28; Fig 4; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide agonists of exendin - delay stomach emptying, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-347456/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agonist peptide SEQ ID NO 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agonist; treatment; antidiabetic; insulin sensitivity; diabetes; lucose; gastric emptying; food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                 L'Italien JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypo- or hyper-glycaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prickett
                                                                                                                                                                                                                                                                                                                             99US-0116380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%;
59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                 Kolterman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70.5;
Pred. No. 3.
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or reducing food intake.

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RESULT 9
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                                                                      RESULT 10
                                                                                                                                              Matches
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                       The present invention relates to extendins and their agonists which have been modified with molecular weight increasing agents such as polyethylene glycol (PEG). These can be used in the treatment of diabetes, obesity, impaired glucose tolerance, postprandial dumping syndrome, postprandial hyperglycaemia, eating disorders, insulin resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
                                                                                                                                                                                                                                                                                                     Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity -
         20-OCT-2000
                                                AAY94184 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia; insulin-resistance syndrome; food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB53029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB53029 standard; Peptide; 36 AA.
                             AAY94184;
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                  Disclosure; Fig 4; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-672834/65.
                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2000; 2000WO-US11814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200066629-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extendin agonist compound #157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                              l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                     4 GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
                                                                                                                        4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GTFTSDASKQLEEEÄVRLFIEFLKNGGPSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                     Prickett K;
                                                                                                                                                                                      36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
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                                                                                                                                              Conservative
         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0132018
                                                                                                                                                     62.9%;
59.4%;
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59.4%;
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                                                                                                                                              0
                                                                                                                                                  Score 70.5; DB 21
Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70.5; DB 21;
Pred. No. 3.2e-06;
                                                                                                                                            Mismatches
                                                                                                                                                                 DB 21;
                                                                                                                                                                 Length 36;
                                                                                                                                              Indels
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                                                                                                                                                                 밁
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                                                                                                                                                                                                                             Query Match
              Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                             Exendin agonist peptide #160.
                                                                    01-NOV-2001 (first entry)
                                                                                                           AAE08515 standard; peptide; 36 AA
                                                                                                                                                                                                                                                    Sequence
                                                                                         AAE08515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heloderma sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of an extendin agonist
                                                                                                                                                                 4
                                                                                                                                                                                                                                                    36 AA;
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The present sequence represents a modified extendin or extendin agonist. Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic crythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4G; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2000; 2000US-0175365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 62.9%;
Local Similarity 59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
                                                                                                                                                                                                                              4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0116380
99US-0132017
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                                                                                                                                                                                                                                                                                                                                                             /note= "amidated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70.5; DB 2:
Pred. No. 3.2e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
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RESULT 12
AAB64351
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                       Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-2001; 2001WO-US00719
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                                                                                   01-JUN-1999;
                                                                                                                                                      07-DEC-2000
                                                                                                                                                                                                                                                                                                                                          Exendin agonist, SEQ ID NO:171
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB64351 standard; peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMYL-) AMYLIN PHARM INC.
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                                                                                                                   23-MAY-2000;
                                                                                                                                                                                        WO200073331-A2
                                                                                                                                                                                                                                        Heloderma suspectum
                                                                                                                                                                                                                                                                                                                                                                                27-MAR-2001
                                                  (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                     2000WO-US14231.
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                                                                                   99US-0323867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%;
59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 70.5; DB 2: Pred. No. 3.2e-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAY24869
8
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Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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cc ability to increase insulin secretion. In contrast, in a normal compensancy, both insulin resistance and insulin secretion in both the mother and the compensancies are associated with complications in both the mother and the compensancies. GDM compensancies of Caesarian delivery. CC hypertensive disorders such as pre-eclampsia, and urinary tract in fections. GDM results in an elevated rate of foetal abnormalities such as natural tract complications. GDM results in an elevated with an increased risk of caesarian delivery. CC hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent conditions of the Gila monster (exendin are peptides from the salivary secretions of the Gila monster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the compounds used to treat type 2 (diabetes, which are contraindicated for GDM, exendins and exendin agonists do not cross the placenta and thus do not cause severe prolonged blood glucose, and, unlike conventional insulin therapy, should not cause between the prolonged compounds as they inhibit gastric emptying and reduce appetite. The present sequence represents a exendin agonist of the invention which is based upon the sequence of exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabetes mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 166; Page 113; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially in a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject.
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36 AA;
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19; 4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34 Similarity GTFTSDASKOLEEEAVRLFIEFLKNGGPSSGA 35 Conservative 62.9%; 59.4%; 0 Score 70.5; Pred. No. 3. Mismatches 3.2e-06 DB 22; Length 36; Indels ۲. Gaps

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Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                                                                                                                                                                                                                                                      Exendin agonist peptide #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1999
                                                                               14-NOV-1997;
                                                                                                                    13-NOV-1998;
                                                                                                                                                                                                      WO9925727-A2
                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY24869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY24869 standard;
                                     (AMYL-) AMYLIN PHARM INC
                                                                                                                                                            27-MAY-1999.
                                                                                                                                                                                                                                             Heloderma
                                                                                                                                                                                                                                         gp.
Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                               97US-0065442
                                                                                                                      98WO-US24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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Best Local :
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AAY24809 to AAY24877 represent exendin agonist peptides which can regulate gastric motility and slow gastric emptying. The peptides can used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic conditions. The peptides are exendin agonists which have activity as agents to regulate gastric motility and to slow gastric emptying, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                    New exendin agonist peptides - can regulate gastric motility slow gastric emptying, used for treating, e.g. diabetes
                                                                                                       Claim 18; Fig 4; 108pp; English
                                                                                                                                                                                            WPI; 1999-394773/33.
                                                                                                                                                                                                                          Beeley NRA,
                                                                                                                                                                                                                                                           (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                           14-NOV-1997;
                                                                                                                                                                                                                                                                                                                          13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                             27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                 W09925727-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              Heloderma sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exendin agonist peptide #45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY24853 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New exendin agonist peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-394773/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastric emptying, used for treating, e.g. diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                          Prickett KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                           97US-0065442
                                                                                                                                                                                                                                                                                                                            98WO-US24210
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    can regulate gastric motility and

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Best Local S
Matches 19
                                       AAY24809 to AAY24877 represent exendin agonist peptides which can regulate gastric motility and slow gastric emptying. The peptides can be used for treating e.g. diabetes or hyperglycaemic or hypoglycaemic conditions. The peptides are exendin agonists which have activity as agents to regulate gastric motility and to slow gastric emptying, as evidenced by the ability to reduce post-prandial glucose levels in mammals. They can be used for the treatment of Type I and II diabetes and hyperglycaemic or hypoglycaemic conditions. They can also be used for the treatment of disorders which would be benefited by agents which lower plasma glucose levels and in treatment of disorders which would be benefited with agents useful in delaying and/or slowing gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evidenced by the ability to reduce post-prandial glucose levels in mammals. They can be used for the treatment of Type I and II diabetes hyperglycaemic or hypoglycaemic conditions. They can also be used for treatment of disorders which would be benefited by agents which lower plasma glucose levels and in treatment of disorders which would be benefited with agents useful in delaying and/or slowing gastric
                                emprying.
                                                                                                                                                                                                                                                    Claim 18; Fig 4; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                          Beeley NRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exendin; agonist; Heloderma sp.; Gila monster; venom; lizard; diabetes mellitus type I; diabetes mellitus type II; hyperglycaemia; hypoglycaemia; plasma glucose; gastric emptying; stomach emptying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                     slow gastric emptying, used for treating, e.g. diabetes
                                                                                                                                                                                                                                                                                                     New exendin agonist peptides
                                                                                                                                                                                                                                                                                                                                         WPI; 1999-394773/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heloderma sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exendin agonist peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9925727-A2
                                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GTXXXXXXXXXXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                          Prickett
                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0065442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US24210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.5; DE L. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.3e
0; Mismatches

    can regulate gastric motility

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Matches Query Match

Local Similarity 19;

62.9%;

Score 70.5; DB zv; Pred. No. 3.3e-06;

Indels Length

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Gaps

Conservative

Sequence

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RESULT 17
AAB53041
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AAB11275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel formulation (I) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat diabetes -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11275,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB11275 standard; Peptide; 37 AA
    Extendin; agonist; diabetes; obesity; eating disorder; dyslipidaemia; insulin-resistance syndrome; food intak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-514584/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2000; 2000US-0116380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200041546-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasma glucose; gastric emptying; food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin; agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exendin agonist peptide SEQ ID NO 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2001
                                                                                                                                           Extendin agonist compound #169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or reducing food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 192; Page 238; 281pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAB53041 standard; Peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTFTSDLSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTFTSALSKQMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L'Italien JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0116380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolterman O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5; DB 21
Pred. No. 3.3e-06;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XSXEXEXEXEXEXEXSXOOOOOXSX
         PRINCE SERVING SERVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to extendins and their agonists which ha been modified with molecular weight increasing agents such as been modified with molecular weight increasing agents such as polyethylene glycol (PEG). These can be used in the treatment of diabetes, obesity, impaired glucose tolerance, postprandial dumping syndrome, postprandial hyperglycaemia, eating disorders, insulin resistance syndrome, dyslipidaemia and to suppress glucagon secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified exendin or an exendin agonist linked to one or more polyethylene glycol (PEG) polymers, modulate plasma glucose levels, useful for treating disorders such as diabetes and obesity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heloderma sp.
14-JAN-2000; 2000WO-US00942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of an extendin agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY94196 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 4; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-2000; 2000WO-US11814.
                                                                                              20-JUL-2000
                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672834/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200066629-A1
                                                                                                                                                                                        WO200041548-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heloderma sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTFTSALSKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prickett K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0132018
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-methyl alanine"
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                            'note= "N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%;
                                                                                                                                                                                                                                                                                  "amidated N-methyl alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 3.3e:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic crythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a modified extendin or extendin agonist. Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification peptides a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is
                             (AMYL-) AMYLIN PHARM INC
                                                         10-JAN-2000; 2000US-0175365.
                                                                                     09-JAN-2001; 2001WO-US00719.
                                                                                                                  19-JUL-2001
                                                                                                                                              WO200151078-A1
                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                      Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                   Exendin agonist peptide #72.
                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                             AAE08427
                                                                                                                                                                                                                                                                                                                                                                                                                        AAE08427 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4G; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMYL-) AMYLIN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2000; 2000US-0175365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GTFTSALSKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                              (first entry)
Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0116380.
99US-0132017.
                                                                                                                                                                                       /note= "N-Methyl-alanine"
37
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                           /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.5; DB 21
Pred. No. 3.3e-06;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 37;
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RESULT 20
AAE08428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                     Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and divertic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                WPI; 2001-514422/56.
                                                                                                                                       Kolterman ⊙G,
                                                                                                                                                                                         10-JAN-2000; 2000US-0175365
                                                                                                                                                                                                                 09-JAN-2001; 2001WO-US00719.
                                                                                                                                                                                                                                                                       W0200151078-A1
                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                           Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exendin agonist peptide #73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE08428 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                  (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                              19-JUL-2001
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE08428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 76; Page 82; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514422/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 AA;
                                             Page 83; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                       Young AA;
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                             /note= "N-Methyl-alanine; C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                                                       note= "N-Methyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.98;
                                                                                                                                                                                                                                                                                                                                               "N-Methyl-alanine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 70.5; DB 22
Pred. No. 3.3e-06;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                      dyslipidemia
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The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They

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RESULT 21
AAE08443
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Matches
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                          Query Match
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                                                                               The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels the present peptide sequence is an agonist of exendin.
                                                                                                                                                                                                                                                                                       WPI; 2001-514422/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exendin agonist peptide #88
                                                                                                                                                                                                                  Example 92; Page 92; 161pp; English.
                                                                                                                                                                                                                                             Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                    Kolterman OG,
                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2000; 2000US-0175365
                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-2001; 2001WO-US00719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200151078-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE08443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE08443 standard; peptide; 37
             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
               Similarity
                                                                                                                                                                                                                                                                                                                                                AMYLIN PHARM INC
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                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                  Young AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
            62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.9%;
59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Homoproline; C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Homoproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Score 70.5; DB 22
Pred. No. 3.3e-06;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5;
Pred. No. 3
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                           DB 22;
                          Length 37;
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Gaps
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  XEXBXFFFX88XXFXEXEXEXEXEXEXEXEXEP7X8X505050505050505050505050505050
                                                      CC ability to increase insulin resistance and insulin screening commandation. In contrast, in a normal compregnancy, both insulin resistance and insulin secretion increase. GDM CC pregnancies are associated with complications in both the mother and the pregnancies. Women with GDM have increased rates of Caesarian delivery, Chypertensive disorders such as pre-eclampsia, and urinary tract confections. GDM results in an elevated rate of foetal abnormalities such as necessarian delivery, as neural tube defects, and is associated with an increased risk of CC neonatal morbidites such as hypoglycaemia, hypocalcaemia, hypomagnesaemia, polycythaemia, hyperbilirubinaemia, and subsequent CC childhood and adolescent obseity. Exendins are peptides from the salivary CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the CC insulinotropic effects. Unlike the compounds used to treat type 2 CC diabetes, which are contraindicated for GDM, exendins and exendin cagonists do not cross the placenta and thus do not cause severe prolonged CC hypoglycaemia in the newborn. They have a potent and prolonged effect on CC hypoglycaemia in the newborn effect on the compounds used to treat type 2 CC diabetes, which are contraindicated for GDM, exendins and exendin cause severe prolonged contrains as they inhibit gastric emptying and reduce appetite. The compound upon the sequence represents a exendin a gonist of the invention which is cause upon the sequence represents a exendin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabete mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 76; Page 67; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heloderma suspectum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB64263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB64263 standard; peptide; 37
                                               based upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200073331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exendin agonist, SEQ ID NO:83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R, Prickett KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTFTSDASKOMEEEAVRLFIEWLKNGGXSSGA 35
                                            the sequence of exendin-4.
37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0323867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes
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Query Match Best Local Similarity

62.9%;

Score Pred.

70.5; DB 22; No. 3.3e-06;

59.4%;

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CC pregnancies are associated with complications in both the mother and the foetus. Women with GDM have increased rates of Caesarian delivery, typertensive disorders such as pre-eclampsia, and urinary tract presents as neural tube defects, and is associated with an increased risk of caesarian delivery, as neural tube defects, and is associated with an increased risk of meanatal morbidites such as hypoglycaemia, hypocalcaemia, childhood and adolescent obseity. Exendins are peptides from the salivary exerctions of the Gila monster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the Gliamonster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the Gilamonster. Only particularly GIP-1, and have similar consolities do not cross the placent and tube do not cause severe prolonged agonists do not cross the placent and thus do not cause severe prolonged thypoglycaemia in the newborn. They have a potent and prolonged effect on blood glucose, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The presents acquence represents a exendin agonist of the invention which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabete mellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin resistance and a diminished ability to increase insulin secretion. In contrast, in a normal pregnancy, both insulin resistance and insulin secretion increase. Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 77; Page 68; 133pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMYL-) AMYLIN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAY-2000; 2000WO-US14231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200073331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heloderma suspectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exendin agonist, SEQ ID NO:84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB64264 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTFTSDLSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prickett KS
  37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetes
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Query Match

62.9%;

Score 70.5;

DB 22;

Length 37;

Sequence

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RESULT 24
AAB64279
                                                CC ability to increase insulin secretion. In contrast, in a normal CC pregnancy, both insulin resistance and insulin secretion increase. CDM CC pregnancies are associated with complications in both the mother and the CC foetus. Women with GDM have increased rates of Caesarian delivery, Chypertensive disorders such as pre-eclampsia, and urinary tract infections. GDM results in an elevated rate of foetal abnormalities such as neural tube defects, and is associated with an increased risk of CC neonatal morbidites such as hypoglycaemia, hypocalcaemia, hypographiams, and subsequent childhood and adolescent obseity. Exendins are peptides from the salivary CC secretions of the Gila monster (exendin-4) and the Mexican beaded lizard (exendin-3) which exhibit homology with several members of the Gila monster (exendin-4) and the Mexican beaded lizard CC glucagon-like peptide family, particularly GIP-1, and have similar insulinotropic effects. Unlike the compounds used to treat type 2 diabetes, which are contraindicated for GDM, exendins and exendin CC insulinotropic effects. Unlike the compounds used to treat type 2 Cdiabetes, which are contraindicated for GDM, exendins and exendin CC hypoglycaemia in the newborn. They have a potent and prolonged effect on blood glucose, and, unlike conventional insulin therapy, should not cause weight gain, as they inhibit gastric emptying and reduce appetite. The CC based upon the sequence of exendin-4 agonist of the invention which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the use of an exendin (AAB64181-B64182) or an exendin agonist (AAB64185-B64368) for treating gestational diabetemellitus (GDM) in a patient. GDM arises during pregnancy, and is due to a combination of increased insulin relations and a diminished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exendin agonist; gestational diabetes mellitus; GDM; insulin resistance; pregnancy complication; neonatal abnormality; blood glucose modulator; insulinotropic; anorectic; exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 92; Page 75; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially in a human -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of exendins or exendin agonists for lowering or reducing blood glucose levels and treating gestational diabetes mellitus in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-137634/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hiles R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200073331-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin agonist, SEQ ID NO:99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB64279 standard; peptide; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTFTSDLSKQMEEEAVRLFIEWLKNGGASSGA
                                      the sequence of exendin-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetes
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RESULT 26
AAY94039
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AAB11311
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Best Local :
                                                                                                                                                                                                                                              Query Match
   Amino acid sequence of an extendin agonist.
                             20-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                  This invention describes a novel formulation (1) comprising an exendin or exendin agonist peptide, a buffer and an iso-osmolality modifier which has a pH of 3-7. The products of the invention have antidiabetic activity. The exendin or exendin agonist is used to increase the sensitivity of a subject to insulin to treat diabetes and disorders which would benefit from agents which lower plasma glucose levels and disorders which would benefit from agents that delay and/or slow gastric emptying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exendin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exendin agonist peptide SEQ ID NO 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11311 standard; Peptide; 39 AA.
                                                                                     AAY94039 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                     or reducing food intake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New formulations comprising an exendin or exendin agonist peptide used for increasing the sensitivity of a subject to insulin to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 42; Figure 15; 281pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-514584/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2000; 2000US-0116380.
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                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucose; gastric emptying; food intake.
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                                                                                                                                                             4,
                                                                                                                                                                                       4 GTXXXXXXXQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTFTSDASKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agonist; treatment; antidiabetic; insulin sensitivity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                             GTFTSDLSKOMEEEAVRLFIEWLKNGGASSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L'Italien JJ,
                                                                                                                                                                                                                                                                             39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.9%;
ilarity 62.5%;
Conservative
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                62.9%;
59.4%;
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                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 11;
                                                                                                                                                                                                                                 Score 70.5; DB 21
Pred. No. 3.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.5; DB 22; Pred. No. 3.3e-06;
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                               Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                   Gaps
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                                                                                                 RESULT 27
AAY94040
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                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                 AAY94013-43 represent extendin agonists, derived from AAY94012. Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-1999; 99US-0116380.
30-APR-1999; 99US-0132017.
10-JAN-2000; 2000US-0175365.
Amino acid sequence of an extendin agonist.
                             20-OCT-2000
                                                                                     AAY94040 standard; peptide; 39
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 3B; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2000; 2000WO-US00942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heloderma sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMYL-) AMYLIN PHARM INC.
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                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                20;
                                                                                                                                                                                       4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                            GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA
                                                                                                                                                                                                                                                                           39 AA;
                                                                                                                                                                                                                   Conservative
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "thioproline'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
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                                                                                                                                                                                                                              62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "thioproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "thioproline"
                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                 Score 70.5; DB 21; Pred. No. 3.5e-06;
                                                                                     8
                                                                                                                                                                                                                                3.5e-06
                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                  1,
                                                                                                                                                                                                                   Gaps
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RESULT 28
AAY94043
                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 20
         Amino acid sequence of an extendin agonist.
                                                                                                                                                                                                                                                                                                                                                                                            AAY94013-43 represent extendin agonists, derived from AAY94012. Excendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma. The method is suffering from reduced glucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
                                                   20-OCT-2000
                                                                                                                       AAY94043 standard; peptide; 39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-1999; 99US-0116380.
30-APR-1999; 99US-0132017.
10-JAN-2000; 2000US-0175365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3B; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-490999/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2000; 2000WO-US00942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extendin; Gila monster lizard; Mexican Beaded lizard; agonist; glucagon-like peptide; plasma glucagon; necrolytic erythema; glucagonoma; hyperglucagonemia; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200041548-A2
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                                                                                                                                                                                                                                                     4 GTXXXXXSKOXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                   GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gedulin B;
                                                                                                                                                                                                                                                                                                                                                                    39 AA;
                                                                                                                                                                                                                                                                                            Conservative
                                                 (first entry)
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99US-0132017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "homoproline"
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "homoproline"
38
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                                                                                                                                                                                                                                                                                                        62.5%;
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0; Mismatches
                                                                                                                                                                                                                                                                                                      .5e-06;
                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                          Indels
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   RESULT 29
AAE08379
ID AAE08
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AC AAE08
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                                                                                                                                                                                                                                                                                                                                                                                    AAY94013-43 represent extendin agonists, derived from AAY94012. Extendins are found in the salivary glands of the Gila monster and Mexican Beaded lizard, and have sequence similarity to glucagon-like peptides. They are used in the method of the invention. The specification describes a method for lowering plasma glucagon, comprising administering an exendin, an exendin agonist, a modified exendin or a modified exendin agonist. These compounds lower plasma glucagon level. The method is useful for lowering plasma glucagon in subjects, preferably humans, suffering from necrolytic erythema or glucagonoma. The method is also useful for treating hyperglucagonemia and other conditions that would benefit from reduced glucagon levels and/or suppression of glucagon, e.g. type 1 and type 2 diabetes.
Exendin agonist peptide #26.
                                     01-NOV-2001 (first entry)
                                                                                                               AAE08379 standard;
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lowering plasma glucagon using exendin, an exendin agonist, a modified exendin or a modified exendin agonist, useful for treating hyperglucagonemia and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JAN-1999; 99US-0116380.
30-APR-1999; 99US-0132017.
10-JAN-2000; 2000US-0175365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3B; 96pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200041548-A2
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                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                             4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                         GTFTSDLSKOLEEEAVRLFIEFLKNGGXSSGA
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                                                                                                             peptide; 39
                                                                                                                                                                                                                                                                                                  62.5%;
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Pred. No. 3.5e-06;
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RESULT 30
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Best Local Similarity
Matches 20; Conserv
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Synthetic
                                                                                          01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of exendin and exendin agonist compounds for modulating triglyceride levels, and treating heart disease and dyslipi
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                        diuretic;
                         Exendin agonist; antilipemic; cardiant; triglyceride; inotropic; diuretic; coronary heart disease; dyslipidaemia.
                                                               Exendin agonist peptide #27.
                                                                                                                                            AAE08380 standard;
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 26; Page -; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514422/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agonist; antilipemic; cardiant; triglyceride; inotropic;
c; coronary heart disease; dyslipidaemia.
                                                                                                                                                                                                           GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                   39 AA;
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                                                                                         (first entry)
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                                                                                                                                            peptide; 39
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Pred. No. 3.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and dyslipidemia
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Search completed: December 23, Job time: 36.5 secs

2003, 10:01:24

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                                                  Matches
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                                                                                                                            The patent discloses a method for modulating plasma or postprandial triglyceride and other lipid levels by administering exendin or an exendin agonist. Exendins have inotropic and diuretic effects. They suppress the secretion of glucagon. Exendin and its agonists have a significant effect on the reduction of blood serum triglyceride concentrations. They are used to treat coronary heart disease and dyslipidaemia, and for modifying postprandial triglyceride levels. The present sequence is an agonist of exendin. Note: The present sequence is not shown in the specification but is derived from SEQ ID NO:3 shown in page 17 of the specification.
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2000; 2000US-0175365
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                                                                                                                                                                                                                                                                                                        triglyceride levels, and treating heart disease and dyslipidemia
                                                                                                                                                                                                                                                                                                                     Use of exendin and exendin agonist compounds for modulating
                                                                                                                                                                                                                                                                                                                                                WPI; 2001-514422/56.
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                      4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                    AMYLIN PHARM INC
                                                                Similarity
GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA
                                                                                                     39 AA;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                          Young AA;
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37
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                                                               Score 70.5; DB 22
Pred. No. 3.5e-06;
                                                   Mismatches
35
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Result
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Maximum Match 10
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
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116.720 Million cell updates/sec
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Query
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Listing first 50 summaries
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Copyright (c) 1993 - 2003
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     US-09-323-867A-183
US-09-323-867A-35
US-09-323-867A-39
US-09-323-867A-67A-69
US-09-323-867A-173
US-09-323-867A-170
US-09-323-867A-184
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Compugen Ltd.
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                 171, App
193, Appl
183, Appl
35, Appl
36, Appl
179, Appl
179, Appl
179, Appl
179, Appl
179, Appl
181, Appl
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	02-596-	-08-066-48	US-08-066-480-1	4-847-1	4	US-09-614-847-101	US-09-323-867A-167	67A-	US-09-323-867A-62	US-09-614-847-140	US-09-614-847-130	US-09-323-867A-64	US-09-614-847-132	US-09-323-867A-66	US-09-323-867A-185	US-09-323-867A-172	-09-323-867A-8	-09-323-867A-	US-09-323-867A-188	US-09-323-867A-37	US-09-323-867A-33	US-09-323-867A-31
equence 9, Appl	equence 7, App	equence 2, Appl	equence 1, Appl	equence 129, Ap	equence 104,	e 101, Ap	equence 167, Ap		ence 62,	Sequence 140, App	e 130,	e 64,	e H	•	Αp	Sequence 172, App	Sequence 87, Appl	8, App	ence 188,	7	ence 33,	Sequence 31, Appl

ALIGNMENTS

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RESULT 2
US-09-323-867A-99
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             Sequence 99, Application US/09323867A
PATENT NO. 6506724
GENERRAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMPLIAND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032.UTL2 (243/131US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USB OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT APPLICATION UNBER: US/09/323,867A
CURRENT FILING DATE: 199-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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      CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
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LOCATION: (36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: artificial sequence with specific variable residues
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                                                                                                                                                                                                                                                                                                                                                                                          Local
APPLICATION NUMBER: US/09/323,867A
                                                                                                                                                                                                                                                                                                                                                                     l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                  GTFTSDASKQLEEEAVRLFIEFLKNGGPSSGA 35
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                        59.4%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 70.5;
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                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      No.
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 36;
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RESULT 4
US-09-323-867A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032,UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 199-06-01
CURRENT FILING DATE: 199-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PATENTIN VET. 2.1 and Microsoft Word
SEQ ID NO 183
LENGTH: 37
LENGTH: 37
Sequence 35, Application US/09323867A Patent No. 6506724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 99
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6506724
GENERAL INFORMATION:
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LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is homoproline
NAME/KEY: MOD RES
LOCATION: (37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (31)
OTHER INFORMATION: Xaa is homoproline
                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Xaa is N-methylalanine NAME/KEY: VARIANT LOCATION: (36)...(37)
OTHER INFORMATION: Xaa is N-methylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: AMIDATION, Position 37 is homoproline-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                 ocal
                                                                                                                                                                                                             20;
                                                                                                                                                                  4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
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                                                                                                                                                                                                                                 Similarity
                                                                                                                            GTFTSALSKOMEEEAVRLFIEWLKNGGXSSGA 35
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                             62.9%;
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                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                               Score 70.5;
Pred. No. 1.
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Pred. No. 1.
                                                                                                                                                                                                                               1.2e-06
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                                                                                                                                                                                                                                                   Length 37;
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                                                                                                                                                                                                             Indels
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US-09-323-867A-36
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TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032.UTLZ (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 36
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APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIRBETES MELLITUS
FILE REFERENCE: 030639.0032 UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 199-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word'
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6506724
GENERAL INFORMATION:
                                               Matches
                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa at position 31 is thioproline NAME/KEY: VARIANT LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is thioproline
                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa at position 31 is homoproline NAME/KEY: VARIANT LOCATION: (36)..(38)
                                                                                                                                                                                  NAME/KEY: MOD_RES
LOCATION: (39)
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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LOCATION: (39)
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ORGANISM: Artificial Sequence
                                                                                                                                                         OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                                                                                                                                                                              CTHER INFORMATION: X
                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: artificial sequence with specific variable residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 39
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                                                                Match 62.9%;
Local Similarity 62.5%;
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Local Similarity 62.5%;
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4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
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                                            Conservative
                                                                                                                                                                                                                              Xaa at positions 36,37, and 38 is homoproline
                                            0; Mismatches
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                                                                Score 70.5; DB 4;
Pred. No. 1.3e-06;
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                                                                                      DB 4;
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                                            Indels
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4 GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35

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                                                                                                                                                                                                                                                                                                   APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 69
LENGTH: 35
TWORE. DET
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TILE REFERENCE: 030639.0032.UTL2 (243/331US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 39
                                                        Query Match
Best Local Similarity
                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                       OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD_RES LOCATION: (35) OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (36)...(38)
OTHER INFORMATION: Xaa at positions 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                              TYPE: PRT
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LOCATION: (39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa at position 31 is N-methylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                            19;
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4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
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                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.5%;
                                                             62.1%; Score 69.5;
59.4%; Pred. No. 1.
                                         <u>0</u>
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Pred. No. 1.
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37, and 38 is N-methylalanine
                                                               1.8e-06;
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                                                                                   DB 4; Length 35;
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                                         Indels
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TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILLING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 173
LENGTW. 7
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US-09-323-867A-67
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Amilin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032,UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/233,867A
CURRENT FILING DATE: 199-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 67
LENGTH: 36
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 173, Application US/09323867A Patent No. 6506724
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67, Application US/09323867A Patent No. 6506724
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                                                                                                                                                                                            OTHER INFORMATION: AMIDATION, Position 36 is Pro-NH2
                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (36)
                                                                                                                                                                                                                                                             OTHER INFORMATION: artificial sequence with specific variable residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD_RES LOCATION: (35)
OTHER INFORMATION: AMIDATION, Position 35 is Ala-NH2
                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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TYPE: PRT
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                                                                                                      Local Similarity
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Local Similarity 59.4%;
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                                      GTXXXXXSKQXEEEAVRLXXXXI-XGGXSSGA 34
GTFTSDLSKQLEEEAVRLFIEFLKNGGPSSGA 35
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                                                                                   Conservative
                                                                                                      59.4%;
                                                                                   0; Mismatches
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                                                                                                                            Score 69.5; DB 4;
                                                                                                      Pred. No. 1.8e-06
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Pred. No. 1.8e-06;
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RESULT 10

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US-09-323-867A-86
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; TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS; FILE REFERENCE: 030639,0032 UTL2 (243/131US); CURRENT APPLICATION NUMBER: US/09/323,867A
; CURRENT FILING DATE: 1399-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 170
LENGTH. 2
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US-09-323-867A-170
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APPLICANT: Amylin pharmaceuticals, Inc.

APPLICANT: Young, Andrew et al.

APPLICANT: Young, Andrew et al.

TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS

FILE REFERENCE: 030639,0032.UTL2 (243/131US)

CURRENT APPLICATION NUMBER: US/09/323,867A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

SOFTWARE: PATENTIN Ver. 2.1 and Microsoft Word

SEQ ID NO 86
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                                                                               Matches
                                                                                                                   Query Match
                                                                                                                                                                                                    OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD RES LOCATION: (36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (36)
OTHER INFORMATION: Xaa is homoproline
                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (36)
OTHER INFORMATION: AMIDATION, Position 36 is homoproline-NH2
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LOCATION: (36)
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Local Similarity 62.5%;
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                                      4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                   Similarity
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GTFTSALSKOMEEEAVRLFIEWLKNGGPSSGA 35
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                                                                                                 62.1%;
59.4%;
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Pred. No. 1.8e-06;
0; Mismatches 11
                                                                                                   Score 69.5;
Pred. No. 1.
                                                                                 Mismatches
                                                                                                   1.8e-06;
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                                                                                                                       DB 4;
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Sequence 184, Application US/09323867A

Patent No. 6506724

GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 184
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US-09-323-867A-184
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US-09-323-867A-65
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; SEQ ID NO 65
TENCTH: 37
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GENERAL INFORMATION:

APPLICANT: Amylin Pharmaceuticals, Inc.

APPLICANT: Young, Andrew et al.

APPLICANT: Young, Andrew et al.

APPLICANT: Young, Exemples and Agonists Thereof for the Treatment TITLE OF INVENTION: OSE OF EXEMBLES AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OSEGSTATIONAL DIABETES MELLITUS

FILE REPERENCE: 030639,0032,UTL2 (243/131US)

FILE REPERENCE: 030639,0032,UTL2 (243/131US)

CURRENT APPLICATION NUMBER: US/09/323,867A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

SOPTWARE: Patentin Ver. 2.1 and Microsoft Word
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LOCATION: (36)
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NAME/KEY: VARIANT
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                      OTHER INFORMATION: AMIDATION, Position 37 is Pro-NH2
                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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TYPE: PRT
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LOCATION: (31)
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OTHER INFORMATION: artificial sequence with specific variable residues
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                                         4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
4 GTFTSDLSKOLEEEAVRLFIEFLKNGGPSSGA 35
                                                                                                           Similarity
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                                                                                                           62.1%;
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                                                                                                              Score 69.5; DB 4; Length 37; Pred. No. 1.9e-06;
                                                                                          Mismatches
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US-09-323-867A-83
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Patent No. 6506724
GENERAL INFORMATION:
APPLICANT: Amylin pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,887A
CURRENT APPLICATION NUMBER: US/09/323,887A
CURRENT FILING DATE: 1399-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word
SEQ ID NO 83
Query Match
Best Local S
Matches 20
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APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REPERENCE: 030639,0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 84
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OTHER INFORMATION: Xaa is N-methylalanine
NAME/KEY: MOD_RES
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                NAME/KEY: MOD_RES
LOCATION: (37)
                                                                                                                                                                        LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is N-methylalanine
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                     Local Similarity
                                                                                                          INFORMATION: AMIDATION, Position 37 is N-methylalanine-NH2
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  Conservative
                  62.1%;
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62.5%;
  0
                  Score 69.5; DB 4;
Pred. No. 1.9e-06;
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Pred. No. 1.
    Mismatches
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                                        DB 4; Length 37;
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US-09-323-867A-63; Sequence 63, Application US/09323867A; Patent No. 6506724
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                                                                      US-09-323-867A-63
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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639-0032.UTLZ (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 85, Application US/09323867A Patent No. 6506724
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                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word SEQ ID NO 63 LENGTH: 38
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Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Amylin Pharmaceuticals, Inc. APPLICANT: Young, Andrew et al.
                                                                                                         OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD_RES LOCATION: (38)
                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (36)..(37)
OTHER INFORMATION: Xaa is homoproline
                                                                                         OTHER INFORMATION: AMIDATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: artificial sequence with specific variable residues
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20; Conserv
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59.48;
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  Score 69.5; DB 4
Pred. No. 1.9e-06
                                                                                         Position 38
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Pred. No. 1.
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                                                                                         is Pro-NH2
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                     DB 4;
                       Length 38;
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Matches

19;

Conservative

<u>.</u>

Mismatches

Indels

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Gaps

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RESULT 18
US-09-323-867A-81
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APPLICANT: Amylin Pharmaceuticals, Inc.

APPLICANT: Young, Andrew et al.

APPLICANT: Young, Andrew et al.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETS MELLITUS

FILE REFERENCE: 030639.0032.UTL2 (243/131US)

CURRENT APPLICATION NUMBER: US/09/323,867A

CURRENT APPLICATION NUMBER: US/09/323,867A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

SOFTWARE: Patentin Ver. 2.1 and Microsoft Word

SEQ ID NO 81
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                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word SEQ ID NO 168
LENGTH: 38
TYPE: PRT
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Best Local Similarity
                     Query Match
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APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXEMULIS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (242/13).US)
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
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OTHER INFORMATION: Xaa is thioproline NAME/KEY: VARIANT LOCATION: (36)...(38)
OTHER INFORMATION: Xaa is thioproline NAME/KEY: MOD RES NAME/KEY: MOD RES LOCATION: (38)
LOCATION: (38)
                                                                                                OTHER INFORMATION: AMIDATION,
                                                                                                                     FEATURE: FEATURE: OTHER HYDORMATION: artificial sequence with specific variable residues NAME/KEY: MOD RES
                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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62.5%;
62.1%;
59.4%;
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Score 69.5;
Pred. No. 1
                                                                                                  Position 38 is Pro-NH2
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  5; DB 4;
1.9e-06;
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                        Length 38;
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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS FILE REFERENCE: 030639.0032 UTL2 (243/131US) CURRENT APPLICATION NUMBER: US/09/323,867A CURRENT FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 189 -06-01 SOFTWARE: PARENTIN VET. 2.1 and Microsoft Word SEQ ID NO 181 LENGTH: 38
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US-09-323-867A-181
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US-09-323-867A-9
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                                                                                                                                                                                      APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT APPLICATION WINDER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09323867A Patent No. 6506724 GENERAL INFORMATION:
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              OTHER INFORMATION: artificial sequence with specific variable residues NAME/KBY: MOD_RES LOCATION: (39) OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (36)..(38)
OTHER INFORMATION: Xaa is thioproline
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: VARIANT LOCATION: (31)
                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 1.9e:
0; Mismatches
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Query Match

Score 69.

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Length 39;

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US-09-323-867A-21
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                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
ITITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,887A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTYARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 21
    Best Loc
Matches
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Matches 19; Conserv
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                    Query Match
Best Local Similarity
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Best Local :
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AIPLICANT: Young, Andrew et al.

AIPLICANT: YOUNG OF EXEMDINS AND AGONISTS THEREOF FOR THE TREATMENT TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS

FILE REFERENCE: 030639.0032.UTL2 (243/131US)

CURRENT APPLICATION NUMBER: US/09/323,867A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189
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                                                                                                                      LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39
NAME/KEY: VARIANT
LOCATION: (10)
                                                                                                                                                                                       OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: MOD RES LOCATION: (39)
                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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LOCATION: (39)
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                                                                                                      OTHER INFORMATION: Xaa is pentylglycine
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Score 69.5; DB 4; Length 39; Pred. No. 2e-06; o; Mismatches 11; Indels
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TITLE OF INVENTION: USE OF EXEMULIS AND AGONISTS THEREOF FOR THE TREATMENT FITLE OF INVENTION: USE OF EXEMULIS AND AGONISTS THEREOF FOR THE TREATMENT CURRENT APPLICATION NUMBER: US/09/323,867A

COURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 189

SOSTWARE: Patentin Ver. 2.1 and Minimum and Minimum
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US-09-323-867A-26
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TITLE OF INVENTION: USE OF EXEMPINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1399-05-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 23
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LOCATION: (39)
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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,887A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 30
LENCTURE OF SEQ ID NOS: 189
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APPLICANT: Young, Andrew et al.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
TILE REFERENCE: 030639,0032.UTL2 (243/531US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTWARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 28
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GENERAL INFORMATION:
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GENERAL INFORMATION:
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LOCATION: (39)
OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Xaa at position 23 is tertiary-butylglycine
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                                          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                          62.1%;
Similarity 59.4%;
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62.5%;
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Pred. No. 2e-06;
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US-09-323-867A-33
US-09-323-867A-33
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APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Young, Andrew et al.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639,0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 189
SOFTMARE: Patentin Ver. 2.1 and Microsoft Word
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/09323867A Patent No. 6506724 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 and Microsoft Word SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09323867A
Patent No. 6506724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity 62.5%;
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TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR THE TREATMENT
TITLE OF INVENTION: OF GESTATIONAL DIABETES MELLITUS
FILE REFERENCE: 030639.0032.UTL2 (243/131US)
CURRENT APPLICATION NUMBER: US/09/323,867A
CURRENT FILING DATE: 1999-06-01
RUMBER OF SEQ ID NOS: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                              NAME/KEY: VARIANT LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (36)..(38)
OTHER INFORMATION: Xaa at positions 36, 36, and 38 is thioproline NAME/KEY: MOD RES
LOCATION: (39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                    OTHER INFORMATION: artificial sequence with specific variable residues NAME/KEY: VARIANT LOCATION: (31)
                     OTHER INFORMATION: AMIDATION, Position 39 is Ser-NH2
                                                                                                                                                                            OTHER INFORMATION: Xaa at position 31 is homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa at position 31 is thioproline
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                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                   LOCATION: (39)
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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Pred. No. 2e-06;
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                                                                                                  37,
                                                                                                     and 38 is homoproline
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Search completed: December 23, 2003, 10:04:28 Job time: 14.5 secs
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US-09-323-867A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 62.1%; Score 69.5; DB 4; Length 39; Best Local Similarity 62.5%; Pred. No. 2e-06; Matches 20; Conservative 0; Mismatches 11; Indels
                                                                                                                                                      Query Match 62.1%; Score 69.5; DB 4; Length 39; Best Local Similarity 62.5%; Pred. No. 2e-06; Matches 20; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09323867A Patent No. 6506724
                                                                                                                                                                                                                                                                    OTHER INFORMATION: artificial sequence with specific variable residues
LOCATION: (31)
OTHER INFORMATION: Xaa at position 31 is N-methylalanine
NAME/KEY: VARIANT
LOCATION: (36)...(38)
OTHER INFORMATION: Xaa at positions 36, 37, and 38 is N-methylalanine
NAME/KEY: MOD RES
LOCATION: (39)
COLUMN TOWN TAXION Docition 30 is Caranto
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                                                                            4 GTFTSDLSKOMEEEAVRLFIEWLKNGGXSSGA 35
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                   Score
                                                            36.5
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40.5
5.5
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284:344 Million cell updates/sec
                                                                                                                                                                                                                                                                                                    Match
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Listing first 50 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     Length
 DB
$53321
JC6198
D75311
A75054
                                      $713352
T13352
T36629
$69070
E86303
C84185
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A69173
T06215
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G85876
A65008
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G97690
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A41520
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T51087
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          alpha-tropomyosin
conserved hypothet
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plastid division p
molybdenum cofacto
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natriuretic peptid
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                                                                             protein
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ALIGNMENTS

R;Eng, J.; Andrews, P.C.; Kleinman, W.A.; Singh, L.; Raufman, J.P.
J. Biol. Chem. 265, 20259-20262, 1990
A;Title: Purification and structure of exendin-3, a new pancreatic secretagogue isolat A;Reference number: A23674; MUID:91056067; PMID:1700785
A;Accession: A23674

exendin-3 - Mexican beaded lizard C;Species: Heloderma horridum (Mexican beaded lizard) C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997

C; Accession: A23674

HWGH3Z

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R;Eng, J.; Kleinman, W.A.; Singh, L.; Singh, G.; Raufman, J.P.
J. Biol. Chem. 267, 7402-7405, 1992
A;Title: Isolation and characterization of exendin-4, an exendin-3 analogue, from Helc A;Reference number: A42486; MUID:92218391; PMID:1313797
A;Accession: A42486
A;Molecule type: protein
A;Residues: 1-39 <ENG-
C;Comment: Exendin-4 does not stimulate amylase secretion by pancreatic acinar cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-39 <ENG>
C;Comment: Exendins are venom components that are thought to bind to receptors for vas
g in secretion of amylase.
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; secretagogue; venom
F;39/Modified site: amidated carboxyl end (Ser) #status experimental
                                                      C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; venom
F;39/Modified site: amidated carboxyl end (Ser) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Heloderma suspectum (Gila monster)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 21-Nov-1997
C;Accession: A42486
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HWGH4G
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Query Match
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 Mismatches

Score 68.5;
DB 1;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-458 <KRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kruse, S.; Kiessling, J.; Harter, K.; Rensing, S.; Decker, E.; Reski, R. submitted to the EMBL Data Library, August 1999
A;Description: Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plastid division protein ftsZ1 [imported] - moss (Physcomitrella patens)
C;Species: Physcomitrella patens
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
transcription regulator, CarD family Atu2765 [imported] - Agrobacterium tumefaciens (str C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 201/3; 301/3; 332/1; 373/3; 404/3; 426/3 C;Superfamily: cell division protein ftsZ C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-464 <KRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kruse, S.; Kiessling, J.; Harter, K.; Rensing, S.; Decker, E.; Reski, R. submitted to the EMBL Data Library, August 1999
A;Description: Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plastid division protein ftsZ2 [imported] - moss (Physcomitrella patens) C;Species: Physcomitrella patens C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000 C;Accession: T51090
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A; Accession: T51089
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A;Accession: T51090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AJ249138; PIDN: CAB54558.1
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                                                                                 AD2916
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Best Local
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Local Similarity 33.3%;
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Local Similarity 33.3%;
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                                                                                                                                                                                GCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGA 212
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                                                                                                                                                                                                                                                                                                        Score 40.5; DE Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                     17;
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                                                                                                                                                                                                                                                                                                                                   Length 464;
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                                                                                                                                          R;Tully, R.E.; Keister, D.L.
Appl. Environ. Microbiol. 59, 4136-4142, 1993
A;Title: Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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  A;Cross-references: EMBL:U12678; NID:g529961; PIDN:AAC28889.1; PID:g529962
                        A; Molecule type: DNA
A; Residues: 1-401 < RES>
                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                    A; Reference number: I40207
A; Accession: I40208
                                                                                                                                                                                                                                                  C;Species: Bradyrhizobium japonicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000
                                                                                                                                                                                                                                                                                                           cytochrome P450 BJ-1 CYP112 - Bradyrhizobium japonicum N_iContains: oxidoreductase (EC 1.-.-.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-189 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-189 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                 C; Accession: I40208
                                                                                                                                                                                                                                                                                                                                                            I40208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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C;Accession: AD2916
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClé, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8. A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium (A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: G97690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, I Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR_C_5013 [imported] - Agrobacterium tumefaciens (strain C58, CrC;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: G97690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm
                                                                                                                                                                                                                                                               A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE007869; PIDN:AAK88480.1; PID:g15157987; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE008688; PIDN:AAL43746.1; PID:g17741280; GSPDB:GN00186
154 NKMSETEAVRLVEVNLAKGPKRG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 NKMSETEAVRLVEVNLAKGPKRG 176
                                                              11 SKQXEEEAVRLXXXXLXGGXSSG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 SKQXEEEAVRLXXXXLXGGXSSG 33
                                                                                                                                                            h 34.8%; Score 39; [
Similarity 43.5%; Pred. No. 7
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Pred. No. 7
                                                                                                                                   Mismatches
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C;Accession: F86457

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G;Genetics:
A;Gene: CYP112
A;Gene: CYP118
C;Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology
C;Kuperfamily: Bacillus cytochrome P450 cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;234-372/Domain: cytochrome P450 homology <CYP>
F;2350/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-468 <ELS>
A;Cross-references: EMBI
                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, February 2000
A;Description: A new cDNA encoding FtsZ-like protein from Nicotiana tabacum
A;Reference number: Z25288
A;Accession: T51087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chloroplast FtsZ-like protein [imported] - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 21-Jull-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T51087
R;El-Shami, M.; Alcaraz, J.P.; Lerbs-Mache, S.; Falconet, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.
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                                                                                                                                                                                                                  A;Cross-references: EMBL:AJ271750; PIDN:CAB89288.1
A;Experimental source: variety Bright Yellow 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-781 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                          ;Keywords: chloroplast
   Query Match
Best Local
                                                                                                                           Superfamily: cell division protein fts2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Local Similarity
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Similarity 50.0%;
9; Conservation
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Pred. No. 32;
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   Score 38.5;
Pred. No. 2
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                              DB 2;
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RESULT 12 G85876

probable transport yfdC [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

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A;Molecule type: DNA
A;Residues: 1-310 <HAYS
A;Ressidues: 1-310 <HAYS
A;Cross-references: GB:BA000007; PIDN:BAB36653.1; PID:g13362700; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3230
   밁
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: F91032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transport ECs3230 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguc. DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transcription initiation factor IIB - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Datc: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Datc: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: F91032
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A;Experimental source: strain OT3
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A; Residues: 1-208 < KAW >
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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguci
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                                                      12 KOXEEEAVRLXXXXXXXGGXSSGA 34
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KELERDAMALLWSAIAAGLSMGA 72
                                                                                                                Conservative
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Pred. No. 19;
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Pred. No.
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C;Accession: G85876
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85876
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A;Accession: A65008

A;Atatus: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-310 <BLAT'>

A;Cross-references: GB:AB000322; GB:U00096; NID:g1788684; PIDN:AAC75407.1; PID:g1788689;

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:
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A;Cross-references: GB:AE005174; NID:g12516714; PIDN:AAG57475.1; GSPDB:GN00145; UWGF:Z3:
A:Experimental source: strain O157:H7, substrain ED1933
                                                                                                                                                                                                                                                          probable membrane protein STY2625 [imported] - Salmonella enterica subsp. enterica serov (.Species: Salmonella enterica subsp. enterica serovar Typhi A.Note: this species has also been called Salmonella typhi (.) Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (.) Accession: AG0805 (.) Accession: AG0805 (.) Agrachill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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                                                                                                           th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.,
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: ABOS02; MUID:21534947; PMID:11677608
A;Accession: AG0805
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                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <PAR>
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Cross-references: GB:AL513382; PIDN:CAD07625.1; PID:g16503616; GSPDB:GN00176;
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Best Local Similarity 34.8%;
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Pred. No. 19;
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Pred. No. 19;
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C;Accession: AI3286

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanoval, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letel Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitely. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription regulator [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fur A;Reference number: A69000; MUID:98037514; PMID:9371463
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A; Residues: 1-207 < KUR>
                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-248 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein MTH552 - Methanobacterium thermoautotrophicum (strain [C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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                                                                                                                                                                     C; Superfamily: hypothetical protein MJ1250
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A;Experimental source: strain Delta H
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                                                                                                                                                                                             ;Gene: MTH552
;Start codon:
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Best Local :
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Local Similarity 43.5%;
Local Similarity 43.6%;
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12 KOXEEEAVRLXXXXLXGG 29
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Pred. No. 20;
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Pred. No. 20;
                                                                                     Pred. No. 24;
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R;Litts, J.C.; Simmons, C.R.; Karrer, E.E.; Huang, N.; Rodriguez, R.L. Eur. J. Biochem. 194, 831-838, 1990
A;Title: The isolation and characterization of a barley 1,3-1,4-beta-glucanase gene. A;Reference number: $13830, MUID:91099365; PMID:2148518
A;Accession: T06215
                                                                                   N;Alternate names: picuitary secretory protein I; secretory protein I N;Contains: chromostatin; pancreastatin C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 18-Aug-2000 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 18-Aug-2000 C;Accession: A41520; A26033; A24175; A60306; A61114; S15847; S39016; I46008; S38976 R;Iacangelo, A.L.; Grimes, M.; Eiden, L.E. Mol. Endocrinol. 5, 1651-1660, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamil C;Keywords:
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A;Molecule type: DNA
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N,Alternate names: endo-1,3-beta-glucanase
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 29-Sep-1999
C;Accession: T06215
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A;Cross-references: EMBL:U96096; NID:g2735501; PIDN:AAC39322.1; PID:g2735502
A;Title: The bovine chromogranin A gene: structural basis for hormone regulation and gen A;Reference number: A41520; MUID:92140395; PMID:1779968 A;Accession: A41520
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A; Residues: 1-356 < KUR>
A; Cross-references: GB: C; Genetics:
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: H90168
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A;Accession: H90168
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Similarity 45.0%;
9; Conservation
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Pred. No. 35;
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A; Residues: 266-310,'H',312-318,'K',320-331
A; Note: 311-Arg and 319-Glu were also found
R; Watkinson, A.; Rogers, M.; Dockray, G.J.
Biochem. J. 295, 649-654, 1993
A; Title: Post-translational processing of ch
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R;Barbosa, J.A.; Gill, B.M.; Takiyyuddin, M.A.; O'Connor, D.T.
Endocrinology 128, 174-190, 1991
A;Title: Chromogranin A: posttranslational modifications in secretory granules.
A;Reference number: A61114; MUID:91099142; PMID:1986917
A;Reference number: A61114; MUID:91099142; PMID:1986917
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R;Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ishida, K.; Makk, G.; Angwin, P.; Chang, D.
Regul. Pept. 25, 207-213, 1989
A;Title: Isolation and characterization of bovine pancreastatin.
A;Reference number: A60306; MUID:89331945; PMID:2756155
A;Accession: A60306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 266-312 < NAK>
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A; Molecule type: DNA
A; Residues: 1-449 < IAC>
                                                     A; Status: not compared with conceptual translation
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A;Cross-references: GB:S79270; NID:g244423; PIDN:AAB21297.1; PID:g244424 R;Ahn, T.G.; Cohn, D.V.; Gorr, S.U.; Ornstein, D.L.; Kashdan, M.A.; Levine, M.A. Proc. Natl. Acad. Sci. U.S.A. 84, 5043-5047, 1987 A;Title: Primary structure of bovine pituitary secretory protein I (chromogranin A) A;Reference number: A28033; MUID:87260925; PMID:3474638 A;Accession: A28033. ŏ

A;Residues: 1-11,'T',113-190,'Y',192-253,'P',255-378,'R',380.449 <ANN>A;Crose-references: GB.M16971; NID:g163727; PIDN:AAA30765.1; PID:g163728 A;Note: the authors translated the codon CGG for residue 391 as Gln R;Iacangelo, A.; Affolter, H.U.; Eiden, L.E.; Herbert, E.; Grimes, M. Nature 323, 82-86, 1986

A,Title: Bovine chromogranin A sequence and distribution of its messenger RNA in endow A,Reference number: A24175; MUID:86311345; PMID:3018587 A;Accession: A24175

A;Accession: A61114

A;Molecule type: protein
A;Molecule type: protein
A;Residues: 19-34,'X', 36-38;97-111;134-139 <BA2>
A;Residues: 19-34,'X', 36-38;97-111;134-139 <BA2>
R;Watkinson, A.; Joensson, A.C.; Davison, M.; Young, J.; Lee, C.M.; Moore, S.; Dockray, Biochem. J. 276, 471-479, 1991
Biochem. J. 276, 471-479, 1991
A;Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and A;Reference number: S15847; MUID:91264803; PMID:1710890
A;Accession: S15847

A;Reference number: \$39016; MUID:94059013; PMID:8240272

A;Molecule type: protein
A;Residues: 303-331 <MAT>
A;Residues: 303-331 <MAT>
R;Benedum, U.M.; Baeuerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.; Hut EMBO J. 5, 1495-1502, 1986
A;Title: The primary structure of bovine chromogranin A: a representative of a class < A;Reference number: 146008; MUID:86300648; PMID:3755681
A;Accession: 146008

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-135,'8',137-190,'Y',192-253,'P',255-310,'H',312-318,'K',320-390,'Q',392.
A;Residues: 1-135,'8',137-190,'Y',192-253,'P',255-310,'H',312-318,'K',320-390,'Q',392.
A;Cross-references: EMBL:X04012; NID:g197; PIDN:CAA27636.1; PID:g198

R;YOO, S.H.; Ferretti, J.A.
FEBS Lett. 334, 373-377, 1993
A;Title: Nature of the pH-induced conformational changes and A;Reference number: S38976; MUID:94063061; PMID:8243650
A;Accession: S38976 exposure of the C-termina

A;Molecule type: protein
A;Residues: 19-26;266-272 <YOO>
A;Residues: 10-26;266-272 <YOO>
C;Comment: Chromogranin A is the major protein of bovine chromaggin granules.
C;Comment: Chromostatin activity has been demonstrated from proteolytic fragments of (C;Genetics: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
C;Superfamily: chromogranin A

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R;Yanaka, N.; Kotera, J.; Taguchi, I.; Sugiura, M.; Kawashima, K.; Omori, K. Eur. J. Biochem. 237, 25-34, 1996
A;Title: Structure of the 5'-flanking regulatory region of the mouse gene encoding the A;Reference number: S71332; MUID:96203905; PMID:8620881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              natriuretic peptide clearance receptor - mouse
N;Alternate names: atrial natriuretic factor clearance receptor
C;Specites: Mus musculus (house mouse)
C;Date: 23.dul-1997 #sequence_revision 01-Aug-1997 #text_change 20-Jun-2000
C;Accession: S71332
R;Yanaka, N.; Kotera, J.; Taguchi, I.; Sugiura, M.; Kawashima, K.; Omori, K.
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S71332
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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-149/product: chromogranin A #status experimental <MAT>
F;142-161/Product: chromostatin #status predicted <MAT3>
F;266-312/Product: pancreastatin #status experimental <MAT2>
F;266-312/Product: pancreastatin #status experimental <MAT2>
                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-850 <KEL>
                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, May 1998
A;Reference number: Z17660
A;Accession: T13352
                                                                                                                                                                                                                                                                                                                                                                                                                                            stn-A protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 17-Nov-2000
C;Accession: T13352
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A; Residues: 1-536 < YAN>
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                                                12 KOXEEEAVRL 21
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                                                                                                Similarity
8; Conserv
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9; Conserv
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  KOKEEEAARL 149
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                                                                                                                     33.0%; Score 37; DB
80.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.0%; Score 37; DB 56.2%; Pred. No. 52; tive 0; Mismatches
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Pred. No. 44;
                                                                                                  Mismatches
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                                                                                                                                                DB 2; Length 850;
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RESULT 22

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C;Accession: E86303

C;Accession: E86303

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein YPR084w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P9513.5
C;Speciaes: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
C;Accession: S69070
R;Couch, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transcription regulator - Streptomyces coelicolor G;Species: Streptomyces coelicolor G;Species: Streptomyces coelicolor G;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999 C;Accession: T3652 #Sequence_revision 03-Dec-1999 #text_change 07-Dec-1999 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-124 <CLI>
A;Cross-references: EMBL:AL078610; PIDN:CAB44397.1; GSPDB:GN00070; SCOEDB:SCH35.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: Z21610
A;Accession: T36629
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F6I1.17 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 16R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YPR084w
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A; Residues: 1-456 < COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: The sequence of S. cerevisiae cosmid 9513 A;Reference number: S69057
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Pred. No. 15;
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Pred. No. 55
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Biochem. J. 303, 915-921, 1994
A;Title: Human cytochrome b(561): a revised hypothesis for conformation in membranes whi
A;Reference number: S53321; MUID:95071309; PMID:7980462
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84185
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A;Residues: 1-144 <STO>
A;Cross-references: GB:AE005172; NID:g9802781; PIDN:AAF99850.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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                                                                                                                            A; Map position: 17q11-17qter
                                                                                                                                                A;Gene: GDB:CYB561
A;Crosm-references: GDB:228138
                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-251 <SRI>
                                                                                                                                                                                                                                                                                                                                                         R;Srivastava, M.; Gibson, K.R.; Pollard, H.B.; Fleming, P.J. Biochem. J. 303, 915-921, 1994
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C;Superfamily: uncharacterized conserved protein
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C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
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A;Residues: 1-249 <STO>
A;Cross-references: GB:AE004437; NID:g10579889; PIDN:AAG18847.1; GSPDB:GN00138
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A;Status: preliminary
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                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                                  Best
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les 8; Conserv
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      QXEEEAVRLXXXXXXGGXSSGA 34
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                                            Conservative
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                                                              32.1%;
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                                                                  Score 36; DB 2; Length 251; Pred. No. 37;
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Pred. No. 21;
                                            Mismatches
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  R; anonymous,
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                                                                                                                          RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: DR2143
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Genoscope
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: A75054
                                                         molybdenum cofactor biosynthesis protein (moea-1) PAB1436 - Pyrococcus abyssi (strain C;Species: Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Map position: 1 C, Superfamily: erythrocyte band 7 integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans FA;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ATmC-2
C;Superfamily: tropomyosin
C;Keywords: actin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA A;Residues: 1-284 <LUQ> A;Residues: 1-284 <LUQ> A;Residues: 1-284 <LUQ> A;Cross-references: GB:U33449; NID:g1871355; PIDN:AAC60091.1; PID:g1871356 C;Comment: This protein is a actin-binding protein. C;Genetics:
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R;Luque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F.
Gene 185, 175-180, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-344 <WHI>
A;Residues: 1-344 <WHI>
A;Cross-references: GB:AE002048; GB:AE000513; NID:g6459929; PIDN:AAF11687.1;
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein - Deinococcus radiodurans (strain R1) c;Species: Deinococcus radiodurans (c;Species: Deinococcus radiodurans (C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: D75311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Differential expression of a novel isoform of alpha-tropomyosin in cardiac A;Reference number: JC6198; MUID:97208870; PMID:9055812 A;Contents: Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Ambystoma mexicanum (axolotl)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-tropomyosin C-2 - axolotl
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es 7; Conserv
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                                                                                                                                                                                                                                                                 232 QAEAEATRVVSQAIAGG 248
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                                                                                                                                                                                                                                                                                                                                                                                                  32.1%; Score 36; DB 2; Length 344;
41.2%; Pred. No. 52;
ative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.1%;
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru A;Reference number: A75001
A;Accession: A75054
A;Status: preliminary
A,Molecule type: DNA
A;Residues: 1-402 < KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50326.1; PID:g545883
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50326.1; PID:g545883
C;Genetice: A;Gene: PAB1436
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thiamine biosynthesis enzyme ThiH [imported] - Clostridium acetobutylicum C.Species: Clostridium acetobutylicum C.Species: Clostridium acetobutylicum C.C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C.Accession: A97067 R.Nolling, J. Breton, G., Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bennett, G.N.; Koonin, E.V.; Smith, D.R. ABACteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MJID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <KUR>
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A97067
Job time : 15.5 secs
                              Search completed: December 23, 2003, 10:02:40
                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CAC1356
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001437; PIDN:AAK79324.1; PID:g15024290; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCCB24
                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                 ;Genetics:
                                                                                                                                                                                                                                                   y Match 32.1%; Score 36; DB 2; Length 472;
Local Similarity 31.8%; Pred. No. 71;
hes 7; Conservative 4; Mismatches 11; Indels
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                                                                                                                            322 SKKTRERVLELGISQISGGSST 343
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Result
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Maximum Match 100%
Listing first 50 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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188.107 Million cell updates/sec
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Match Length DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1262
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TF2B PYRAB
TF2B PYRHO
FFLIG PSEAE
FLIG PSEAE
EMXA HUMAN
ASSY SHEON
IDS MOUSE
MILLN MOUSE
MILLN MOUSE
MILLN RAT
LMG2 MOUSE
MYO6 HUMAN
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Y 4WA RHICH
CKS 1 HUWAN
CKGA BOVIN
ANFC MOUSE
VU79 HSV6U
SP4 HUWAN
NUCI NEUCR
CARB SUTCO
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FOSZ BACSU
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EXE4_HELSU
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P26349 heloderma s
Q59203 bradyrhizob
P37327 escherichia
P55679 rhizobium s
026652 methanobact
059131

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P70180
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O yersinia pe
6 macaca mula
7 leptospira
4 rhizobium s
7 mycobacteri
0 rattus norv
                                                                                                                                                                                                                                                                                                                                         5 pyrococcus
1 pyrococcus
4 pseudomonas
2 homo sapien
8 shewanella
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9 rhizobium s
2 methanobact
7 homo sapien
9 bos taurus
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ì	VP19_HSV2H	VP19_HSV2G	RECA_FUSNN	LPLA ECOLI	YE85 MYCPN	SYGA_WIGBR	TXNL HUMAN	RK16_GRATE	TAGB_DICDI	KF1C HUMAN	KF1D_RAT	LI10_CAEEL	CNRC_CHICK	HR96 DROME	Y552_HUMAN	ENV_MLVMO	Y886_METJA
	P89461 herpes	herpes	Q8rfy0 fusobacter	P32099 escherichia	P75300 mycoplasma	Q8d1w3 wiggleswort	043396 homo sapien	P16633 gracilaria	P54683 dictyosteli	043896 homo sa	035787 rattus	017583 caenorhabdi	gallu	Q24143 drosophil	060299 homo sapien	P03385 moloney mur	Q58296 methanococo
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ALIGNMENTS

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RESULT 2 EXE4_HELSU STANDARD; PRT; 87 AA. ID EXE4 HELSU STANDARD; PRT; 87 AA. AC P26349; DT 01-MAY-1992 (Rel. 22, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update)	.3e-06; es 12; A 34 A 35	HSSP; P01275; 1BH0. InterPro; IPR000532; Glucagon. Pfam; PF00123; hormone2; 1. SMART; SM00070; GLUCA; 1. SMART; SM00070; GLUCA; 1. PROSITE; PS00260; GLUCAGON; 1. Glucagon family; Toxin; Amidation. Glucagon family; Toxin; Amidation. MOD RES 39 SEQUENCE 39 AA; 4204 MW; A44251D3A4B1D1B9 CRC64; SOURTY Match 61.2%; Score 68.5; DB 1; Length 39	RL J. Biol. Chem. 265:20259-20262(1990). CC -:- FUNCTION: Has a VIP/secretin-like biological activity. CC -:- With the exendin receptor. CC -:- SUBCELLULAR LOCATION: Secreted. CC -:- TISSUE SPECIFICITY: Expressed by the venom gland. CC -:- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY. DR DIR. A23674: HMGH3Z.	OC Heloderma. OX NCBI_TaxID=8552; OX NCBI_TaxID=8552; RN [1] RP SEQUENCE. RC TISSUB-Venom; RC TISSUB-Venom; RC TISSUB-Venom; RT MEDLINE=91056067; PubMed=1700785; RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman JP. RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman JP. RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman JP. RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman JP. RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman JP. RA Eng J., English Company (1998) RE T.	STANDARD; PRT; 39 AA. (Rel. 17, Created) (Rel. 17, Last sequence update) (Rel. 41, Last annotation update) (Rel. 41, Last annotation beaded lizard) Metazoa; Chordata; Craniata; Vertebrata; ia; Squamata; Scleroglossa; Anguimorpha;
	Indels 1; Gaps 1;	ingth 3	ctivity. Interacts	ay Cr Cr). ; Buteleostomi; Helodermatidae;

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Eng J., Kleinman W.A., Singh L., Singh G., Raufman J.-P.;
Eng J., Kleinman W.A., Singh L., Singh G., Raufman J.-P.;
"Isolation and characterization of exendin-4, an exendin-3 analogue,
from Heloderma suspectum venom. Further evidence for an exendin
receptor on dispersed acini from guinea pig pancreas.";
J. Biol. Chem. 267:7402-7405(1992).
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"Tissue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.";
J. Biol. Chem. 272:4108-4115(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Heloderma.
                                                                                                                  CPXP_BRAJA STANDARD; PRT; 401 AA (59203; 01-NOV-1997 (Rel. 35, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat 15-SEP-2003 (Rel. 35, Created) (Cytoch CYP112 OR BLR2144 (CYP112 OR BL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucagon family; Toxin; Amidation; Signal; 3D-structure.
SIGNAL 1 23 POTENTIAL.
PROPEP 24 47
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-!- FUNCTION: Has a VIP/secretin-like biological activity.
-!- with the exendin receptor.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
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                                       Bradyrhizobiaceae; Bradyrhizobium
                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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[nterPro; IPR000532; Glucagon.
    TaxID=375;
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59.4%;
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C_ECÓLI STANDAR YFDC ECOLI STANDAR 73737; 01-OCT-1994 (Rel. 30, 01-OCT-1994 (Rel. 30, 28-FEB-2003 (Rel. 41, Hypothetical protein YFDC OR B2347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T., Nakamura Y., Sato S., Mi
Sasamoto S., Watanabe A., Idesawa K
Kohara M., Matsumoto M., Shimpo S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tully R.E., van Berkum P., Lovins K.W., Keister D.L.; "Identification and sequencing of a cytochrome P450 gene cluster from Bradyrhizobium japonicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japonicum that is expressed anaerobically and
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
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                                                                                                                                                                                                                                                                                                SEQUENCE
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Pfam; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
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PROSITE; PS00086; CYTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Environ. Microbiol. 59:4136-4142(1993).
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10; Conserv
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be A., Idesawa K., Iriguchi M.,
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                                               Last sequence update)
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Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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E -> Q (IN REF. 1 AND 2).
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                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Construction of a contiguous 874-kb sequence of the Bscherichia - K12 genome corresponding to 50.0-68.8 min on the linkage map ar analysis of its sequence features.";
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Submitted (JUN-1994)
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Enterobacteriaceae; Escherichia.
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               Y4WA
                                                                                                                                                                                                                                                                                              Hypothetical SEQUENCE 3:
                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000323; AAC75407.1; -.
EMBL; D90865; BAA16207.1; -.
EMBL; U11296; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474\,(1997).
                                                                                     Y4WA_RHISN
P55679;
                                                                                                                     RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished observations (AUG-1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
 Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION.
                            lypothetical
                                                                                                                                                                                                                                                                                                                                          A65008; A65008
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                                                                                                                                                                              KELERDAMALLWSAIAAGLSMGA
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                                                                                                                                                                                                                                                                                               al protein;
310 AA; 3
                                          (Rel.
(Rel.
                                                                                                                                                                                                                                      Conservative
(strain NGR234)
                                                                                                       STANDARD;
                           41, Last annotation update) protease y4wA (EC 3.4.99.-).
                                          35, Created)
35, Last sequence update)
41, Last annotation updat
                                                                                                                                                                                                                                                                                                   34503 MW;
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                                                                                                                                                                                                                                                    33.9%;
                                                                                                                                                                                                                                                                                               Complete proteome.
4503 MW; 96D34F450B209ED3 CRC64;
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                                                                                                                                                                                                                                                                   Score 38;
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                                                                                                        512
                                                                                                                                                                                                                                                                    DB 1; Length 310;
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Matches 9
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SITE
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PCrB protein homolog.
PCRB OR MTH552.
Metharological PCRB OR MTH552.
                                                                                                                                                                                                                                                                                                                           PCRB_METTH
026652;
30-MAY-2000
MEDLINE=98037514; PubMed=9371463; Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobia
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97305956; PubMed=9163424;
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                                                                                                                                                                                                               Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria;
Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16. SIMILARITY: TO Y4WB.
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                                                                                                                                                                                                   TaxID=187420;
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PF05193; Peptidase_M16_C; 1.
TE; PS00143; INSULINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TXXXXXSKQXEEEAVRLXXXXLXGGXSS 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 AA;
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135
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Pred. No.
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
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ZINC (BY SIMILARITY)
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          RC TISUE=Brain, and Lung;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Alausner R.D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Coquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Alausner R.D., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RX Alausner R.D., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RX Alausner R.D., McEwan M., McKernan M., Madan A., Rodrigues S., Sanchez A.,

RX Alausner R.D., McEwan M., McGrenn E.D., Dickson M.C.,

RX Alausner R.D., McEwan R.D., Wickson M.C.,

RX Alausner R.D., McEwan M., McEwan R.D., McC.,

RX Alausner R.D., McEwan M., McGrenn E.D., Dickson M.C.,

RX Alausner R.D., McEwan R.D., Wickson M.C.,

RX Alausner R.D., McEwan M.C.,

RX Alausner R.D., McEwan R.D., McEwan R.D.,

RX Alausner R.D., McEwan R.D., McEwan R.D.,

RX Alausner R.D., McEwan R.D., McEwan R.D.,

RX Alausner R.D., M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C561_HUMAN STANDARD;
C561_HUMAN STANDARD;
C94947; Q9BUO5; Q9BWR9;
C1-FEB-1996 (Rel. 33, Created)
C8-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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InterPro; IPR003009; FMN_enzyme
InterPro; IPR002911; PCrB.
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-!- SIMILARITY: Belongs to the porB family.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Srivastava
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TIGRFAMs; TIGR00265; TIGR00265; 1.
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38.9%;
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EMBL; U29461; AAC50212.1; JOINED.
EMBL; U29461; AAC50212.1; JOINED.
EMBL; U29464; AAC50212.1; JOINED.
EMBL; U29469; AAC50212.1; JOINED.
EMBL; U29469; AAC50212.1; JOINED.
EMBL; BC000021; AAH00021.1; -.
EMBL; BC0002976; AAH02976.1; -.
EMBL; U06715; AAA59952.1; -.
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STIVESTAVA M., Gibson K.R., Pollard H.B., Fleming P.J.;
"Human cytochrome b561: a revised hypothesis for conformation in membranes which reconciles sequence and functional information.";
Biochem, J. 303:915-921(1994).

1- FUNCTION: SECRETORY VESICLE-SPECIFIC ELECTRON TRANSPORT PROTEIN.

1- FUNCTION: BINDS TWO HEME GROUPS NON-COVALENTLY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        GG; GO:0005887; C:integral to plasma membrane; TAS.
GG; GO:0005804; C:secretory vesicle membrane; TAS.
GG; GO:0005803; C:secretory vesicle; TAS.
GG; GO:0004128; F:cytochrome b5 reductase activity; TAS.
GG; GO:0006091; P:energy pathways; TAS.
InterPro: IPR004877; Cyt B561.
InterPro: IPR004593; Cyt_b561_fer_ox.
Pfam; PF03188; Cytochrome_B561; 1.
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                                                                                                                                  CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                   Electron transport;
DOMAIN 1
TRANSMEM 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM;
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Genew; HGNC:2571; CYB561.
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-1- SIMILARITY: BELONGS TO THE EUXARYOTIC B561 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
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QAEEQALSMDFKTLTEGDSPGS 250
                             OXEEEAVRLXXXXXXGGXSSGA 34
                                                           Conservative
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                                                                          33.0%;
36.4%;
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CMGA_BC
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01-NOV-1988 (Rel. 09, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Chromogranin A precursor (CgA) (Fituitary secretory protein I) (SP-I)
[Contains: Vasostatin-1; Chromostatin; Chromacin; Pancreastatin; WE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of bovine chromogranin A: a representative a class of acidic secretory proteins common to a variety of
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"The bovine chromogranin A gene: structural basis for hormone regulation and generation of biologically active peptides."; mol. Endocrinol. 5:1651-1660(1991).
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Bovidae; Bovinae; Bos.
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Galindo E., Rill A., Proc. Natl. Acad. Sc
                                                                                                              Galindo E., Rill A., Bader M.-F., Aunis D., "Chromostatin, a 20-amino acid peptide derived f inhibits chromaffin cell secretion.", proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 19-45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromogranin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primary structure of bovine pituitary secretory (chromogranin A) deduced from the cDNA sequence... proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
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Iacangelo A., Affolter H.-U., Eiden
"Bovine chromogranin A sequence and
in endocrine tissues.";
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                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of the secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kang Y.K., Yoo S.H.
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J., Huttner W.B.;
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                                                                                                                                                                                                                                                OF 142-161,
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                                                                                                                                                                                                                                                   AND SYNTHESIS OF CHROMOSTATIN
     Bader M.-F., Aunis D.;
i. U.S.A. 91:832-832(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
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and distribution of its messenger RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ornstein D.L., Kashdan M.A.,
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Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin Chang D., Tatemoto K.; "Isolation and characterization of bovine pancreastatin.";
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SEQUENCE OF 266-312.
MEDLINE=89331945; PubMed=2756155;
MEDLINE=89331945; Mivanaka
                                                                                                                                                                                                                                                                             Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przy "Chromogranin A from bovine adrenal medulla: molecular characterization of glycosylations, phosphorylations,
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"Mechanism of action of chromogranin A on catecholamine release: molecular modeling of the catestatin region reveals a beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.; "Mechanism of cardiovascular actions of the chromogranin A fragment catestatin in vivo.";
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Gill B.M., P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Chromaffin granules; MEDLINE=97067080; PubMed=8910482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regul. Pept. 25:207-213(1989)
                                                                                                                                                                                                      heterogeneities by mass spectrometry.";
Anal. Biochem. 274:69-80(1999).
-!- FUNCTION: Pancreastatin strongly inhibits
release from the pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt strand/loop/beta-strand} structure secured by hydrophobic interactions and predictive of activity.";
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                                                                                                                                                                                                                                                                                                                                  CARBOHYDRATE-LINKAGE SITES, PHOSPHORYLATION, AND MEDLINE=99459228; PubMed=10527498;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lugardon K., Raffner R., Goun
Aunis D., Metz-Boutigue M.-H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20219105; PubMed=10753865;
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                                                                                                                                                                                                                                                                                                                                                                                                           terminal
                                                                                                                                                                                                                                                                                                                                                                                                                               "Antibacterial and antifungal activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION OF VASOSTATIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides 19:1241-1248(1998).
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competitive nicotinic cholinergic antagonist.

FUNCTION: Vasostatin-1 has antibacterial activity against Grampositive bacteria M.luteus, B.megaterium. Not active against Grampositive bacteria B.cereus, B.subtilis, S.pyrogenes, M.fortuitum, S.aureus and L.monocytogenes and against Gram-negative bacteria
                                                                                        FUNCTION: Chromacin has antibacterial activity against M Not active against E.coli.

FUNCTION: Catestatin inhibits catecholamine release from chromaffin cells and noradrenergic neurons by acting as
                                                                                                                                                                                     FUNCTION: Chromostatin completely inhibits catecholamine release
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                                                                                                                                                                     chromaffin cells.
                                                                                                                                                                                                                                                                                                                                                                                           fragment of chromogranin A.";
Chem. 275:10745-10753(2000).
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                                                                                                                                                   against M.luteus
                                                                                                                                                                                                                          induced insulin
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 ANPC MOUSE STANDARD; PRT; 536 AN
P70180; P97804; Q9R025; Q9R027; Q9R028;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
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PROSITE; PS00423; GRANINS_2; 1.
Signal; Amidation; Glycoprotein;
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InterPro; IPR001990; Granin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.coli, E.cloacae, S.typhimurium, K.pneumoniae and P.auruginosa. Possesses antifungal activity against N.crassa, A.fumigatus, A.brassicola, N.hematococca, F.culmorum and F.oxyporum and against S.cereviase and C.albicans yeast. Inactive against T.mentagrophytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.
MISCELLANEOUS: Binds calcium with a low-affinity.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
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1N2Y; 13-NOV-02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01271; Granin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00659; CHROMOGRANIN
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Antibiotic; Fungicide.
                                                                                                                                                                                                          Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     CHROMACIN.
PANCREASTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                    VASOSTATIN-1. CHROMOSTATIN.
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EMBL, U72676; AND PROBLEM BL, U72676; AND PIR; S71332; S71332.

MGD; MGI:97373; NDr3.

A InterPro; IPRO01828; ANF receptor.

R InterPro; IPRO01170; Ntpep_receptorN.

R Pfam; PF01094; ANF receptor; I.

PR PRINTS; PR00255; NANPEPFUIDER.

DR PROSITE; PS00458; ANP RECEPTORS; 1.

PACEPTOR; Glycoprotein; Transmembrane PACEPTOR; Glycoprotein; POTENTIA.

Transmembrane; Signal. POTENTIAL

EMBL; AF131861; AAF00104.1; -.
EMBL; AF131862; AAF00105.1; -.
EMBL; AF131864; AAF00107.1; -.

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15-SBP-2003 (Rel. 42, Last annotation update)
Atrial natriuretic peptide clearance receptor precursor (ANP-C)
(ANPRC) (NPR-C) (Atrial natriuretic peptide C-type receptor) (EF-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fu X., Kamps M.P.; Fu X., Kamps M.P.; each expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yanaka N., Kotera J., Taguchi I., Sugiura M., Kawashima K., Omori "Structure of the 5'-flanking regulatory region of the mouse gene encoding the clearance receptor for atrial natriuretic peptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c; TI
MEDLINE=96203905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Cell. Biol. 17:1503-1512(1997).
-i- FUNCTION: RECEPTOR FOR ATRIAL NATRIURETIC PEPTIDE. DOES NOT HAVE
GUANYLATE CYCLASE ACTIVITY.
-i- SUBUNIT: Homodimer; disulfide-linked (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 96:10278-10283(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99398699; PubMed=10468599;
Jaubert J., Jaubert F., Martin N., Washburn L.L., Lee
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.com/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/license/li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97184476; PubMed=9032278;
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EMBL; D78175; BAA11241.1; -.
                                                                                                           entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

DISEASE: Defects in NPR3 are the cause of a number of skeletal-
newsprowth phenotypes, Longjohn (Lgj), Longjohn 2J (Lgj-2J) and overgrowth phenotypes, Longjohn (Lgj), Longjohn 2J (Lgj-2J) and strigosus (Stri). These are all recessive conditions characterized by an elongated body, thoracic kyphosis, arachnodactyly, and sacral and/or tail kinks, but no significant changes in cranicfacial structures.

CIRCILATION THERE SEEM TO BE AT LEAST THREE ANP RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CIRCILATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

SIMILARITY: TO ANP-A AND ANP-B RECEPTOR IN THEIR EXTRACELLULAR AND SIGNAL TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEMBRANE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biochem. 237:25-34(1996).
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05; PubMed=8620881;
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                                                                                                                                                                       noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Matches
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Protein U79.
U79 OR EDRF1.
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CONFLICT
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CONFLICT
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CARBOHYD
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes.";
Virology 204:738-750(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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EMBL; U13194; AAA68470.1; -.
EMBL; X83413; CAA58371.1; -.
EMBL; X83413; CAA58371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
01-OCT-1996
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                                                                                                                                                                                                                                                                            Virology 209:29-51(1995).
-!- FUNCTION: POSSIBLE REPLICATION PROTEIN.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER
-HSV-7 U79 AND HCMV UL112 (P34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=95266321; PubMed=7747482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                              Gompels U.A., Nicholas J., Lawrence G., Jones M., Thom
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95027704; PubMed=7941342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10370;
                                                                                                                                                                                                                                                                                                                                                                                      "The DNA sequence of human herpesvirus-6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    genome evolution.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HSV6U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conserv
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479
500
103
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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389
66
168
58
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81
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132
293
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LSSING (IN LGJ-2J).

- N (IN LGJ).

DS -> IT (IN REF. 1).

E -> G (IN REF. 1).

G -> V (IN RFF.
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
ATRIAL NATRIURETIC PEPTIDE CLEARANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22E14B5C454F4427 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA
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                                                                                                                                                                                                                                                                                                                                                                                                  structure, coding content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomson B.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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RESULT 11
SP4_HUMAN
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Best Local Similarity
Thehes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SP4_HUMAN STANDARD; PRT; 784 AA Q02446; C60402; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Transcription factor Sp4 (SPR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03064; U79 P34; 1.
SEQUENCE 344 AA; 39272 MW; E34F1FE7ADB7D790 CRC64;
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hagen G., Mueller S., Beato M., Suske G.; "Cloning by recognition site screening of proteins: a family of 5pl related genes.", Nucleic Acids Res. 20:5519-5525(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ozersky P., Holmes A.;
Submitted (APR-1998) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteit
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
DNA-binding; Nuclear protein; Repeat.
ZN_FING 647 671 C2H2-TYPE 1.
ZN_FING 677 701 C2H2-TYPE 2.
                                                pfam; PF00096; zf-C2H2; 3.
probom; PD000003; Znf_C2H2; 2.
swART; SM00355; ZnF_CZH2; 3.
proSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
proSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription_regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                  MIM; 600540; -.
GO; GO:0003702; F:RNA polymerase II transcription factor acti.
GO; GO:0003713; F:transcription co-activator activity; TAS.
GO; GO:0006557; P:regulation of transcription from Pol II pro.
InterPro; IPR007087; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93087156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                     Genew; HGNC:11209; SP4.
                                                                                                                                                                                                                                                                                     PIR; S26638; S26638.
                                                                                                                                                                                                                                                                                                       EMBL; AC004595; AAD12226.1; -.
                                                                                                                                                                                                                                                                                                                     EMBL; X68561; CAA48563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 3 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                         TRANSFAC;
                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [SSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitted (ADR-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Binds to GT and GC boxes promoters elements. Probably transcriptional activator.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: ABUNDANT IN BRAIN.
SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 EÒSHÉDGITLTSTTLVNGAVEGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 KOXEEEAVRLXXXXLXGGXSSGA 34
                                                                                                                                                                                                                                                                       P08047;
                                                                                                                                                                                                                                                     T02339; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1454515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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CONFLICT
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DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUC1_NEUCR
P20824;
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphorus acquisition controlling protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                       use by non-profit institutes Institute. There are no restrictions on modified and this statement is not removed. Usage by and for commercentities requires a license agreement (See http://www.i-h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyc
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUCR
                                                                                                                            PIR; A363/0, ...
HSSP; P07270; 1AOA.
TRANSFAC; T01642; -.
InterPro; IPR001092; HLH_basic.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                 acquisition in Neurospora crassa.";
Mol. Cell. Biol. 10:5839-5848(1990).
--i- FUNCTION: FACTOR THAT ACTIVATES THE TRANSCRIPTION OF STRUCTURAL
--i- SUBUNIT: Binds DNA as a dimer.
--i- SUBUNIT: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa
                                                                                                                                                                                                                                                                       This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                   Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91042513; PubMed=2146493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                    EMBL; M37700; AAA33603.1; -.
                                               DOMAIN
                                                                                             PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
DNA-binding; Transcription
SEQUENCE
            DOMAIN
                                   DOMAIN
                                                                      NIMMOC
                                                                                                                                                                                                                                                                                                                                                                                                    s., Metzenberg R.L.;
ecular analysis of nuc-1+, a gene controlling phosphorus
                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION FACTORS.
                                                                                                                                                                                        A36378; A36378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KQXEEEAVRLXXXXLXGGXSS 32
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122
185
197
197
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            718
                                     468
                                               434
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  AΑ;
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380
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  87275 MW;
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                                                                                             regulation; Nuclear protein; Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ALA.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB pred. No. 51;
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HA -> QP (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE 3.
POLY-GLU.
                        ASP-RICH (ACIDIC).

GLN-RICH (INVOLVED IN TRANSCRIPTIONAL ACTIVATION) (POTENTIAL).

PRO-RICH.

INTERACTION WITH NEGATIVE REGULATORY FACTOR (POTENTIAL).
   HELIX-LOOP-HELIX MOTIF (BY SIMILARITY)
5E513ED989666E2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> A (IN REF. 2).
3C4EAE28CB2B81FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        823 AA
                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                         (ACIDIC).
(INVOLVED IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 784;
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ALUAR REPRESENTATION X SERVICE SERVICE
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                                                                                                                                                                                                 EMBL; AP000986; BAB66576.1; -.

HANNAP; MF 01210; -; 1.

InterPro; IPR005275; CGAR_L_glu.

InterPro; IPR005483; CPASe_L_D.

InterPro; IPR005480; CPASe_L_D.

InterPro; IPR005481; CPASe_L_D.

InterPro; IPR005481; CPASe_L_N.

Pfam; PF00289; CPASSE_L_D2; 2.

Pfam; PF02787; CPSASE_L_D3; 1.

PRINTS; PR00098; CPSASE_L_D3; 1.

PRINTS; PR00098; CPSASE_L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-JCM 10545 / 7;
MEDLINE-21456156; PubMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Nagai Y., Nishijima K., Ctsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oghima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) carbamoyl-phosphate synthase large chain (EC phosphate synthetase ammonia chain).

CARB OR ST1504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 8:123-140(2001).
-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http:\bar{//www}.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                              PROSITE; PS00866; CPSASE 1; 1.

PROSITE; PS00867; CPSASE 2; 1.

Arginine biosynthesis; Pyrinidine biosynthesis; Ligase; Repeat;
                             ATP-binding; Manganese; Complete proteome.
DOMAIN 1 399 CARBOXYPHOSPH
                                                                                                                                                                                'IGRFAMs; TIGR01369; CPSaseII_lrg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphate + L-glutamate + carbamoyl phosphate.
COFACTOR: Binds 3 manganese ions per subunit (By similarity).
PATHMAY: Arginine biosynthesis.
PATHMAY: Pyrimidine biosynthesis; first step.
SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CARB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the large (or ammonia) chain to synthesize carhamoyl phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    765 NKRAEEAERKLVEMKMOGGAATGS 788
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29.2%;
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Pred. No.
      OLIGOMERIZATION DOMAIN
                                CARBOXYPHOSPHATE SYNTHETIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 823;
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MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein (Contains: N-terminal protein (Pl); Helper
component proteinsee (EC 3.4.22.45) (HC-Pro); Protein PJ; 6 kDa
protein 1 (KI); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
protein 1 (KI); Cytoplasmic inclusion protein A (NI-A)
(KI); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
(NIA) (EC 3.4.22.44) (49 kDa proteinsee) (49 kDa-Pro); Nuclear
inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
(EC 2.7 7.48); Coat protein (CP)].
Pepper mottle virus (California isolate) (PeMV) (PepMoV C).
Viruses; serna positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vance V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.; "The complete nucleotide sequence of pepper mottle virus genomic RNA: comparison of the encoded polyprotein with those of other sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q01500;
01-OCT-1993
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   - - -
                                                                                                                                                                                                                                                                                                                                                                      -I- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTECTYTIC ACTIVITY.

-I- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY.

MAY BE INVOLVED IN REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 191:19-30(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             potyviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93033110; PubMed=1413501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=31737;
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CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own terminus, commonly in the sequence "Tyx-Xaa-Val-Gly-|-Gly, processing of the potyviral polyprotein.

produced its covalently linked to the Genomic RNA. Profit VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.

SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C4. SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4. SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                              FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY. CATALYTIC ACTIVITY: Hydrolyzes glutaminyl bonds, and activity is further restricted by preferences for the amino acids in P6 - P1' that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and
                                                                                                                                                                                                                                also cleaved
                                                                                                                                                                                                                                                 oligopeptides containing the appropriate consensus sequence are
                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEMVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 SKKLEEEGIRL 656
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ATP (POTENTIAL).
ATP (POTENTIAL).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
MANGANESE 3 (BY SIMILARITY).
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Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN. ALLOSTERIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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ROCOGEDATA

FTSZ

Bacteria; Firmicutes; NCBI_TaxID=1423;

Bacillales; Bacillaceae; Bacillus.

Bacillus subtilis.

RESULT 15 FTSZ_BACSU

FTSZ_BA

BACSU

STANDARD;

382 AA

01-NOV-1990 01-DEC-1992

(Rel. 16, (Rel. 24, (Rel. 41,

28-FEB-2003

division protein

fteZ

Last annotation Created) Last

sequence update)

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                                               Query Match
Best Local S
Matches 8
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Pfam; PF00271; helicase_C4; 1.

Pfam; PF00863; Peptidase_C6; 1.

Pfam; PF00851; Peptidase_C6; 1.

Pfam; PF00767; Poty_Coat; 1.

Pfam; PF001877; Poty_P1; 1.

Pfam; PF01877; PRTY_P1; 1.

Pfam; PF00680; RNA_dep_RNA_pol; 1.

PRINTS; PR00966, NIRPOTYPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                           SMART; SM00487; DEXDc; 1.
SMART; SM00490; HELICG; 1.
SMART; SM00490; HELICG; 1.
Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
Hydrolase; Transferase; Thiol protein-RNA linkage; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001456; Peptidase C6.
InterPro; IPR001592; Poty_coat.
InterPro; IPR002540; Poty_Pl.
InterPro; IPR007995; RNA_pol_DS PS.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR007994; RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO01410; DEAD.
InterPro; IPRO01650; Helicase_C.
InterPro; IPRO01730; Peptidase_C4.
InterPro; IPRO01456; Peptidase_C6.
InterPro; IPRO01592; Poty_Coat.
                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M96425; AAA46903.1; -.
                                                                                                                                                                                                                                                                               Coat protein
ATP-binding.
                                                                                                                                        BINDING
                                                                                                                                                     CHAIN
                                                                                                                                                                CHAIN
                                                          Match 32.1%;
Local Similarity 80.0%;
87 KQREEEEVRL
                       12 KQXEEEAVRL
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1791
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                                                             Score 36; DB 1;
Pred. No. 2.2e+0
                                                                                                               ATP
                                                                                                                                                               NUCLEAR INCLUSION PROTEIN
                                                                                                                                                                                                     CYTOPLASMIC INCLUSION PROTEIN 6 kDa PROTEIN 2.
                                                                                                                                                                                                                                                                    N-TERMINAL PROTEIN
                                                                                                                                      COVALENT LINKAGE OF VIRAL RNA
                                                                                                                                                                                         GENOME-LINKED PROTEIN
                                                                                                                                                                                                                                           PROTEIN P3
                                                                                                                                                                                                                                                         HELPER COMPONENT
                                                                                                                                                                                                                              kDa PROTEIN 1
                                                  Mismatches
                                                                                                                            SIMILARITY).
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                                                                                                                 (POTENTIAL)
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RX MEDLINE=98044033; PubMed=9384377;
RX MEDLINE=98044033; PubMed=9384377;
RA Azevedo V. Bertero M.G., Messieres P., Bolotin A., Borchert S.,
RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier D., Connection I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connection I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connection I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connection I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connection I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connection I.F., Cummings N.J., Daniel R.A.,
RA Glims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holeappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Lee S.M., Levine A., Liu H., Masuda S., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Raparro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Raparro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Raparro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Raparro V., Pohl T.M., Portetelle D., Rose M., Sadaie Y.,
RA Raparro V., Pohl T.M., Portetelle B., Rose M., Sadaie Y.,
RA Raparro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Raparro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Raparro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Raparro V., Pohl T.M., Portetelle D
                                                                                                                                                                                                                                                                                                                                                                                                   Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.;

"Cloning, genetic organization, and characterization of a structural gene encoding bacillopeptidase F from Bacillus subtilis.";

J. Biol. Chem. 265:6845-6850(1990).

It seems to assemble into a dynamic ring on the inner surface of the cytoplasmic membrane at the place where division will occur, and the formation of the ring is the signal for septation to begin. Binds to and hydrolyzes GTP (By similarity).

-!- SUBCHILLAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).

-!- SUBCLULAR LOCATION: Cytoplasmic. Assembles at the inner surface of the cytoplasmic membrane (By similarity).
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"Cloning and characterization of Bacillus subtilis homologs of Escherichia coli cell division genes ftsZ and ftsA.";
J. Bacteriol. 170:4855-4864(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
                      EMBL; J05400; AAA83361.1; -.
PIR; I39848; I39848.
HSSP; Q57816; IFSZ.
SubtiList; BG10232; ftsZ.
                                                                                                                       EMBL; M22630; AAA22457.1; -. EMBL; Z99111; CAB13402.1; -.
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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IPR000158; FtsZ

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  RESULT 16
TF2B_PYRAB
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PIR; E75110; E75110.
HSSP; P29095; IAIS:
HAMAP; MF 00383; -; 1.
InterPro; IPR006670; CYClin.
InterPro; IPR008812; TFIIB euk.
Pfam; PF00382; transcript fac2; 2.
PRINTS; PR00685; TIFACTORIIB.
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TIGRPAMS; TIGR00065; ftsZ; 1.
PROSITE; PS01134; FTSZ-1; 1.
PROSITE; PS01135; FTSZ-2; 1.
Cell division; Septation; GTP-
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Pfam; PF00091; tubulin;
Pfam; PF03953; tubulin_(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; Van integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.", Mol. Microbiol. 47:1495-1512 (2003).

Mol. Microbiol. 47:1495-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TF2B PYRAB STANDARD; PRT; 300 AA G9V0V5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Transcription initiation factor IIB (TFIIB) TFB OR PYRAB06850 OR PAB1912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Every the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                         PRINTS; PRO0685; TIFACTORII SMART; SM00385; CYCLIN; 2. PROSITE; PS00782; TFIIB; 2.
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27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 5:55-76(1998).

-!- FUNCTION: STABILIZES TBP BINDING TO AN ARCHAEAL BOX-A PROMOTER. ALSO RESPONSIBLE FOR RECRUITING RNA POLYMERASE II TO THE PRE-INITIATION COMPLEX (DNA-TBP-TFIIB) (BY SIMILARITY).

-!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

-!- SIMILARITY: Belongs to the TFIIB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I. Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Masuchi Y., Shizuya H., Kikuchi H.; Horikoshi K., Wasuchi Y., Shizuya H., Kikuchi H.; Masuchi Y., Yamazaki J., Wasuchi Y., Yamazaki J., Wasuchi Y., Masuchi Y., Wasuchi Y., Yamazaki J., Kikuchi H.; Masuchi Y., Kikuchi H.; Masuchi Y., Kikuchi H.; Masuchi Y., Wasuchi Y., Yamazaki J., Wasuchi Y., Wasuchi Y., Yamazaki J., Wasuchi Y., Wasuchi Y., Yamazaki J., Wasuchi Y., Yamazaki Y., Yamazaki J., Wasuchi Y., Yamazaki Y., Yamazaki Y., Yamazaki Y., Yamazaki Yamazaki Y., Yamazaki Y., Yamazaki Yamazaki Y., Yamazaki Y., Yamazaki Y., Yamaza
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30-MAY 2000 (Rel. 39, Created)
30-MAY 2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
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InterPro; IPR006670; Cyclin.
InterPro; IPR006812; TFIIB euk.
InterPro; IPR006812; TFIIB.
Ffam; PF00382; transcript fac2;
PRINTS; PR00685; TIFACTORIIB.
SMART; SM00385; CYCLIN; 2.
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29
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40.9%;
                                                                                                                                                                                         Repeat; Zinc-finger; Metal-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                             ZN-RIBBON
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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on update) (TFIIB).
                                                                                                                                                TFIIB-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLIG PSI
Q51464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lin R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Arora S.K., Ritchings B.W., Almira E.C., Lory S., Ramphal R.;
"Cloning and characterization of Pseudomonas aeruginosa filf,
necessary for flagellar assembly and bacterial adherence to mucin.";
Infect. Immun. 64:2130-2136(1996).

-I- FUNCTION: FILIG IS ONE OF THREE PROTEINS (FLIG, FLIM) THAT
FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE
OF THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLIG OR PA1102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flagellar motor switch protein flig.
                                                                                                                          EMBL; AE004540; AAG04491.1; -.
EMBL; L43507; AAB06802.1; -.
PIR; G83508; G83508.
HSSP; Q9WY63; 10C7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Complete proteome. SEQUENCE 338 AA;
                                  PRINTS; PR00954; FLGMOTORFLIG.
TIGRFAMs; TIGR00207; fliG; 1.
Chemotaxis; Flagella; Flagellar rotation; Inner membrane;
                                                                                            InterPro; IPR000090; Flg_Motor_Flig
Pfam; PF01706; FliG-C; 1.
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96239027; PubMed=8675317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Pseudomonas aeruginosa PAO1,
                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE FLIG FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUENCE OF 1-228 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 KHVEEEAARLYREAVRKGLIRG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 KOXEEEAVRLXXXXXXXGGXSSG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34097 MW;
  37007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.2%; Score 35; 40.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ب</u>
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  81BFBB136B4D1FA1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                        Q8TEI2; Q8TEI1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
LIM homeobox transcription factor 1 alpha (LT
LMX1A) (LIM-homeobox protein 1.1) (LMX-1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, expression and genomic structure of human LMXIA, and variant screening in Pima Indians.";
Gene 290:217-225(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22057902;
                                                                                                                                                                              EMBL; AY078398; AAL82892.1; EMBL; AY078391; AAL82892.1; EMBL; AY078392; AAL82892.1;
                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 homeobox domain.
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MXA HUMAN
                                                                                                                                                                                                                                                      entities requires a
                                           Genew; HGNC:6653; LMX1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Acts as a transcriptional activator by binding to an A/T-rich sequence, the FLAT element, in the insulin gene promoter. Required for development of the roof plate and, in turn, for specification of dorsal cell fates in the CNS and developing vertebrae (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q8TE12-2; Sequence=VSP 003112; TISSUE SPECIFICITY: Isoform 1 is expressed in many tissues. Not found in heart, liver, spleen and testis. Relatively highly expressed in fetal brain. Isoform LMXIA-4B is expressed in testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (By similarity). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=LMX1A-4AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
                              600298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F., Wolford J.K., Wang J., German M.S., Bogardus C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDKANNLIDRILLGGSTSG 111
   IPR001356; Homeobox IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY PubMed=12062816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%;
                                                                                                                                                                                                                                                        latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Pred. No. 33;
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RESULT 20
ASSY_SHEON
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PROSITE; PSG0027; HOMEOBOX 2; 1.

PROSITE; PSG00478; LIM_DOWAIN 1; 2.

PROSITE; PSG0023; LIM_DOMAIN 2; 2.

PROSITE; PSG0027; Nuclear 1.
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Q8EK28;
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SMART; SM00132; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000010; Homeobox; ProDom; PD000094; LIM; 2.
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                                                                                                                                                                                                                              MEDINE-2229/686; PubMed=12368813;
MEDINE-2229/686; PubMed=12368813;
Medine-2229/686; Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Read T.D., Eisen J.A., Seshadri R., Ward N., Brinkac L., Daugherty S., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Medby R.T., Dodson R.J., Durkin A.S., White O., Wolf A.M., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Lee C., Vanathevan J., Weldman J., Impraim M., Lee K., Berry K., Lee C., Waller J., Xhouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venerer J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Argininosuccinate synthase (BC 6.3.4.5) (Citrulline--aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHEON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
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                                                                                                                       Nat. Biotechnol. 20:1118-1123(2002).

-!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP + diphosphate + L-argininosuccinate.

-!- PATHMAY: Arginine biosynthesis; seventh step.

-!- SUBUNIT: Homotetramer (By similarity).

-!- SUBUNIT: Belongs to the argininosuccinate synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARGG OR SO0278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 7; Conservat
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                                                                                                                Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oneidensis.
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33 92
92 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gammaproteobacteria; Alteromonadales;
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GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform LMX1A-4AB)
/FTId=VSP_003112.
; 55424762757FF5FD_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                             a collaboration MBL outstation -
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RESULT 21
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InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
TIGRFAMS; TIGR00032; argG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.

SEQUENCE 407 AA; 44538 MW; ABCABCECE33E4345 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE015476; AAN53363.1; ^.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           sulfatase gene.";
Genomics 16:755-757(1993).
-!- FUNCTION: REQUIRED FOR THE LYSOSOMAL DEGRADATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93315172; PubMed=8325651;
Daniele A., Faust C.J., Herman G.E., di Natale P., Ballabio A.;
"Cloning and characterization of the cDNA for the murine iduron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q08890;
01-OCT-1994
                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Iduronate 2-sulfatase precursor (EC 3.1.6.13)
CHAIN
MOD_RES
                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
                                                                          MGD; MGI:96417; Ids.
InterPro; IPR000917; Sulfatase.
Pfam; PF00884; Sulfatase; 1.
PROSITE; PS00523; SULFATASE 1; 1.
PROSITE; PS00149; SULFATASE_2; 1.
                             PROPEP
                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                              SULFATE AND DERMATAN SULFATE
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                                                                                                                                                     A47153;
                                                                                                                                                                  L07921; AAA37880.1; -.
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8; Conserv
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                                                            Glycoprotein;
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   99
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993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.2%;
                                                             Lysosome; Zymogen; Signal.
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Pred. No. 40;
   POTENTIAL.
BY SIMILARITY.
IDURONATE 2-SULFATASE.
2-AMINO-3-OXOPROPIONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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      ACID
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RA Strausberg R.D., Peingold E.A., Grouse L.H., Derge J.G.,
RA Altacher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altacher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altacher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altacher R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., McDwan P.J., McKernan R.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Sanailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;
RGeneration and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
Tanai H., Kimata M., Watanabe M., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ULG3; Q9NSK4; Q9NUS8;
Q9ULG3; Q9NSK4; Q9NUS8;
28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, L
15-SEP-2003 (Rel. 42, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari
Masuho Y., Kanehori K.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MKIN1) gene to human chromosome 7q32 and physical mapping and FISH."; Cytogenet. Cell Genet. 87:19-21(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         waskerin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams J.C., Zhang L.; "cDNA cloning of human muskelin and localisation of the muskelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20108780;
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(Rel. 41, Last sequence up)
(Rel. 42, Last annotation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12477932;
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63437 MW;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ
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) (POTENTIAL).
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[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 320-735 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF047489; AAF06698.1;
EMBL; AK002024; BAA92042.1;
EMBL; BC002834; AAH02834.1;
EMBL; AL162071; CAB82407.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50897; CTLH; PROSITE; PS50896; LISH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01344; Kelch; 3.
SML.RT; SM00668; CTLH; 1.
SMART; SM00667; LisH; 1.
OB9050;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
                                                                             MKLN MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Binds with the C-terminal tail of the prostaglandin EP3 receptor alpha isoform (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Contains 5 Kelch repeats.
SIMILARITY: Contains 1 LisH domain.
SIMILARITY: Contains 1 CTLH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 CTLH domain.
CAUTION: Ref.2 sequence differs from that shown due to a stop codon in position 171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).
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                                                                                                                                                                                                                                                                                                                                                Similarity
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IPR006652; Kelch_rep.
IPR006594; LisH.
                                                                                                                                                                                                                                                                                                                                                                                                                                    735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :7109; MKLN1
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                                                                                   STANDARD;
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330
391
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ALT_INIT.
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KELCH 3.
KELCH 4.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                   Score 35; DB
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1A8F06FE1DE9193D CRC64;
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                         735 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 735;
                                                                                                                                                                                                                                                                                                                                  2; Indels
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                                                                                                                                                                                                                                                                                                                                     Gaps
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                 RA Strausberg R.D., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Woczean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
Tennal Ra Rodriguez CDNA sequences.";
RT Mannan and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams J.C., Seed B., Lawler J.;
"Muskelin, a novel intracellular mediator of cell adhesive and cytoskeletal responses to thrombospondin-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vėrtebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as iven ... Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement (See http://www.isb-sib.ch/announce/
                                                                                              DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC013703; AAH13703.1; -. MGD; MGI:1351638; Mkln1.
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                                                                       REPEAT
                                                                                                                                                                                                         PROSITE; PS50897; CTLH; PROSITE; PS50896; LISH;
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SMART; SM00667; LisH;
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InterPro; IPR006594; LisH.
                                                                                                                                                                                                                                                                                                                 ofam; PF01344; Kelch;
                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR006595; CTLH
                                                                                                                                                                               repeat;
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MIN:

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RESULT 23

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Matches Query Match Best Local :

CONFLICT CONFLICT

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Best Local
             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99PV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hasegawa H., Katoh H., Fujita H., Mori K., Negishi M.; "Receptor isoform-specific interaction of prostaglandin EP3 receptor with muskelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLN1 OR MSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLN_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -|- SUBCELULLAR INCATION: Cytoplasmic (By similarity).
-|- SUBCELULLAR INCATION: Cytoplasmic (By similarity).
-|- SIMILARITY: Contains 5 Kelch repeats.
-|- SIMILARITY: Contains 1 LisH domain.
-|- SIMILARITY: Contains 1 CTLH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 276:350-354(2000).
-!- FUNCTION: Acts as a mediator of cell spreading and cytoskeletal responses to the extracellular matrix component thrombospondin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND INTERACTIO MEDLINE=20462961; PubMed=11006128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
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15-SEP-2003
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                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                         Pfam; PF01344; Kelch;
SMART; SM00668; CTLH;
                                                                                                                                                                                                                                                     PROSITE; PS50897; CTLH; 1.
PROSITE; PS50896; LISH; 1.
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR006595; CTLH.
InterPro; IPR006652; Kelch_rep.
InterPro; IPR006594; LisH.
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                     Kelch repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity res 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 SKOXEEEAVRL 21
                                                                                                                                                                                                                                                                                         SM00667; LisH;
           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKYREQEAIRL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526
735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                     735 AA;
             Conservative
                                                                                                                                                                                                                                     Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                         204
258
330
391
458
515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84877 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND INTERACTION WITH EP3-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.2%; Score 35; DB 63.6%; Pred. No. 75; tive 2; Mismatches
                                                                                     84833 MW;
             31.2%; Score 35; DB 1; Length 735; 63.6%; Pred. No. 75; cive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KELCH 5
                                                                                                       LISH.
CTILH.
KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7B0C8D2CB8C242AA CRC64;
                                                                                       79BD0BBF74419E76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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밁
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"Short arm region of laminin-5 gamma2 chain: structure, mechanism of processing and binding to heparin and proteins.";

J. Mol. Biol. 314.751-763(2001).

C. FUNCTION: Binding to cells via a high affinity receptor, laminin to thought to mediate the attachment, migration, and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

C. e. SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each cend. The gamma-2 chain is a subunit of laminin-5 (epiligrin/kalinin/nicein) and binds fibulin-1, fibulin-1c, fibilin-2 and nidogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Laminin gamma-2 chain precursor (Kalinin/nicein/epiligrin 100 kDa subunit) (Laminin B2t chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q61092;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAMC2
                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Yamada Y.;
Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiyama S., Utani A., Yamada S., Kozak C.A., Yamada Y.; "Cloning and expression of the mouse laminin gamma 2 (B2t) chain, a subunit of epithelial cell laminin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARG-78; PHE-202; LYS-206
STRAIN=FVB; TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING TO HEPARIN; FIBULIN AND NIDOGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 228:120-128(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMG2 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95188894; PubMed=7882992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=FVB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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EMBL; U43327; AAA85256.2;
                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 laminin IV domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21592560; PubMed=11733994;
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: EPITHEDIAL CELLS OF MANY TISSUES, PARTICULARLY HIGH LEVELS IN TONGUE, HAIR FOLLICLES AND KIDNEY. BASEMENT MEMBRANES OF THE COLLECTING TUBULES OF KIDNEY AND PANCREAS. DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE. DOMAIN: DOMAIN IV IS GLOBULAR.

MISCELLANEOUS: Binds heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).
                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 SKYREQEAIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Goehring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYS-206; CYS-442 AND CYS-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W., Mann K., Brakebusch C., Yamada Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   laminin EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND MUTAGENESIS OF ARG-76;
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Query Match
Best Local Similarity
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DOMAIN
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SMART; SM00180; EGF Lam; 7.
PROSITE; PS00022; EGF-1; 4.
PROSITE; PS01186; EGF-2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 6.
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DOMAIN
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Basement Membrane, Account Repeat; Signal; Laminin EGF-like domain; Cell adhesion; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00052; laminin_B; Pfam; PF00053; laminin_EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:99913; Lamc2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR006209; EGF like.
InterPro; IPR000034; Laminin_B.
InterPro; IPR002049; Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                   SEQUENCE
                                                                                                                                                                                                                MUTAGEN
                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                        1191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
1104
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139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602
1191
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786
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4470
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5314
5338
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     31.2%;
                                                                           130160 MW;
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EGF; 5.
                                                                                                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL ATTACHMENT SITE (POTENTIAL)
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAMININ EGF-LIKE 1.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 4 (N-TERMINAL).

LAMININ DOMAIN IV.

LAMININ EGF-LIKE 5.

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
       Score 35; DB 1;
Pred. No. 1.2e+02;
                                                                                                                                               BINDING
                                                                                                                                                                     FIBULIN-2 BINDING
C->S: 20-FOLD RED
                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular matrix; Coiled coil;
                                                                           7016C1F851D909B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                     NO FIBULIN-1C BINDING. NO CHANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N EGF-LIKE 8 (INCOMPLETE)
II AND I.
COIL (POTENTIAL).
                                                                                                                          20-FOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAMMA-2 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                          REDUCTION
                                                                                                                                                                        REDUCTION TO FIBULIN-2
                              Length 1191,
                                                                                                                          TO FIBULIN-2
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16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avraham K.B., Hasson T., Sobe T., Balsara B., Testa J.R., Skvorak A.B., Morton C.C., Copeland N.G., Jenkins N.A.; "Characterization of unconventional MYO6, the human homologue gene responsible for deafness in Snell's waltzer mice."; Hum. Mol. Genet. 6:1225-1231(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYO6_HUMAN
Q9UM54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21375673; PubMed=11468689;
Melchionda S., Ahituv N., Bisceglia L., Sobe T., Glaser F.,
Rabionet R., Arbones M.L., Notarangelo A., Di Iorio E., Carella M.,
Zelante L., Estivill X., Avraham K.B., Gasparini P.;
"MYO6, the human homologue of the gene responsible for deafness in
Snell's waltzer mice, is mutated in autosomal dominant nonsyndromic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS.
Avraham K.B.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     MEDLINE=99447046; PubMed=10519557; Wells A.L., Lin A.W., Chen L.-Q., Safer D., Cain S.M., Hasson Carragher B.O., Milligan R.A., Sweeney H.L.; "Myosin VI is an actin-based motor that moves backwards.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE=97402203; PubMed=9259267;
                         EMBL; U90236; AAC51654.2;
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 401:505-508(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT DFNA22 TYR-442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin VI
                                                                                                                                                                                           SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                          sensorineural deafness.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
              HGNC:7605; MYO6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKOXEEEAVRLXXXXLXGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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MIM; 600970; -.

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       RESULT 27
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Best Local S
Matches
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16-OCT-2001
16-OCT-2001
28-FEB-2003
Myosin VI
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                                                                                                                                                                                                                           MEDLINE-56083582; PubMed=7493015;
MEDLINE-56083582; PubMed=7493015;
Marcham K.B., Hasson T., Steel K.P., Kingsley D.M., Russell L.B.,
Mooseker M.S., Copeland N.G., Jenkins N.A.;

"The mouse Shell's waltzer deafness gene encodes an unconventional myosin required for structural integrity of inner ear hair cells.";
Nat. Genet. 11:369-375(1995).
Nat. Genet
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00015; IQ; 1.
SMART; SM00042; MYSG; 1.
PROSTIE; PSS0096; IQ; FALSE NEG.
MYOSIN; ATF-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0016461; C:unconventional myosin; TAS.
GO:0003779; F:actin binding activity; TAS.
GO:0005524; F:ATP binding activity; NAS.
GO:00055307; F:structural constituent of muscle; NAS.
                                                                                                                                                            SIMILARITY: Contains 1 myosin-like globular head domain. SIMILARITY: Contains 1 IQ domain.
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8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KOCEEEAERL 926
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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848
151
665
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158
672
442
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80.0%;
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Pred. No. 1.3e+02;
Pred. No. 1.3e+02; Indels
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C -> Y (IN DENSO.
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CF1FA35796FC1C60 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1262;
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RESULT 28
YH74_YERPE
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Best Local
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SEQUENCE
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                                                                                                                                                                                STRAIN:CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L.,

Parkhill J., Wren B.W., James K.D., Churcher C., Mungall K.L.,

Basker S., Basham D., Bencley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Cyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).
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Pfam; PF00063; myosin_head; 4.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8ZFEO;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Hypothetical protein YPO1774/Y2534.
YPO1774 OR Y2534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00015; IQ; 1.
SMART; SM00245; MYSc; 1;
PROSITE; PS50096; IQ; FALSE NEG.
Myosin; ATP-binding; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
       "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                  Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew (Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., EPERTY R.D.,
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YH74_YERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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InterPro; IPR001609; myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:104785; Myo6.
                                                                                                                           SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 KOQEEEAERL 929
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8; Conservat
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849
151
668
766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL) ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.3e+02;
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                                                                                                               Boutin A., Mayhew G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1265;
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Best Local
                                             EMBL; M37572; AAA36922.1; JOINED.
EMBL; M37561; AAA36922.1; JOINED.
EMBL; M37562; AAA36922.1; JOINED.
EMBL; M37563; AAA36922.1; JOINED.
EMBL; M37564; AAA36922.1; JOINED.
EMBL; M37570; AAA36922.1; JOINED.
EMBL; M37571; AAA36922.1; JOINED.
EMBL; M37571; AAA36922.1; JOINED.
EMBL; M37571; AAA36922.1; JOINED.
PIR; S01378; ISMQTR.
HSSP; P00938; IHTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ414150; CAC90592.1; -.
EMBL; AD013856; AAM86090.1; -.
EIR; AD0216; AD0216.
HAMAP; MF 00507; -; 1.
InterPro; IPR005371; UPF0181.
InterPro; UPF0181; 1.
HYDOThetical protein; Complete proteome.
HYDOTHOLICAL PROTEIN; 3EC4ADCA53F29ABE CRC64;
SEQUENCE 85 AA; 9720 MW; 3EC4ADCA53F29ABE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MACMU
                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-rBB-2003 (Rel. 41, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990
28-FEB-2003
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 16:9055-9055(1988).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01d S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPIS_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of the triosephosphate isomerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89016592; PubMed=3174447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9544;
               InterPro; IPR000652; Triophos_ismrse.
Pfam; PF00121; TIM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     \tilde{\mathbf{p}}_{ATH}\tilde{\mathbf{m}}_{AY}; plays an important role in several metabolic pathways SUBUNIT; Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SKOXEEEAVRLXXXXLXGGXSSG 33
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8; Conserv
 PD001005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mohrenweiser H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 14, Created)
(Rel. 14, Last sequence update)
(Rel. 41, Last annotation updat
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Triophos_ismrse; 1
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Pred. No. 12;
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(See http://www.isb-sib.ch/announce/
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Query Match
Best Local Similarity
Matches 7; Conserv

Conservative

Score 34; DB Pred. No. 51;

Mismatches

9; Indels

0

Gaps

0

338 AA;

37839 MW; 30,4%;

70517B5A85ABDA44 CRC64;

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Matches
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ACT SITE 169
ACT SITE 169
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PROSITE; PS00171; TIM; 1.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
MEDLINE=22598143; PubMed=12712204;
Miao Y.-C., Viang Y.-G., Zeng R., Miao Y.-G., Jiang H.-Q., Jia J., Tu Y.-F.,
Zhang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
"Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
Nature 422:888-893(2003).
-I-CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
-I-CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-xmnnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ARGC_LEPIN STANDARD; PRT; 338 AA.
p59307;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (Indept)
acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)
ARGC OR LA2178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                        use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.ich.or send an email to licensease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPIN
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restricted by the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                  + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
-!- PATHWAY: Arginine biosynthesis; third step.
-!- SIMILARITY: Belongs to the NAGSA dehydrogenase family. Subfamily
                   Pfam; PF03118; Semialdhyde_dh; 1.
Pfam; PF03118; Semialdhyde_dhC; 1.
Pfam; PF02774; Semialdhyde_dhC; 1.
ProDom; PD003765; AGPR_act_site; 1.
PROSITE; PS01224; ARGC; FALSE PROSITE; PS01224; ARGC; FALSE PROSITE; PS01224; ARGC; FALSE PROSITE; Complete proteome Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome ACT_SITE 148 148 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=173;
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                                                                                                                                                           EMBL; AE011388; AAN49377.1; -.
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22 SRQKEHEVVHITSDKLAG 39

Search completed: December 23, 2003, 10:01:59 Job time : 11 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	80	7	6	υ	4	ω	N	1	Result
38	38	38	38	38	38	38.5	38.5	39	39	39	39	40	40.5	40.5	41	Score
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P81799	Q06821	Q9X8X6	Q981Z6	Q9DWB5	Q24211	Q9W5M8	Q8PYJ7	Q9R027	Q9F3D1	Q96TC7	Q9NVQ6	Q96SD6	CM086D	050007	Q96H23	Q9H6G1	BOLYBO	Q8FYU2	P89451	Q8XZE5	Q9HBE1	Q9JMG9	Q9UDU0	Q8RM05	Q9Y529	Q9P1A9	Q9HBE2	Q9HBE3	Q8KLD9	Q9HD72	094021	Q8Z4Y7	Q8ZNA4	
EST/33 ISTCHS HOTA	sacchar	deras	TILI ZODIUM	Q9dwbb rac cycomeg	rosopnila	rosopni	me	mus muscui	strepto	omo sapien	ides omoi	como sapi	entrotopo	norded	romo sapi	como sapre	Druceria	pruceria	ř	raiscon	omo sapien	Bru	omo sapre	anthobac	OMC.	omo sapi	omo sapa	Omo sapre	III ZODIUM	כוויס ממעיני	omo cana	Satisticite ta	ıα	201-00011

ALIGNMENTS

RESULT 1 Q8GE53

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Q8GE53; Q1 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Aspartate carbamoyltransferase (EC 2.1.3.2) (Fragment).
Heliobacillus mobilis.
Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Liolios K.G., Chu L., Ostrovskaya O., Mendybaeva N., Koukharenko V.,
Gerdes S., Kyrpides N., Overbeek R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142765; AAN87369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y., Blankenship R.E.;
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                                                                                                                                                                                                                                                                                                     SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome analysis of photosynthetic prokaryotes.";
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324 AA; 35294 MW; 18993D4AE336CD37 CRC64;
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RESULT 3

Q9LDK5

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Matches 12
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kruse S., Kiessling J., Harter K., Rensing S., Decker E., Reski R.; "Two distinct nuclear-encoded plant ftsZ-genes are highly conserved, both their encoded proteins are importedinto chloroplasts and both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                        O9LDK5,
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Plastid division protein ftsZ2 precursor.
FTSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00091; tubulin; 1.
Pfam; PF03953; tubulin C; 1.
PRINTS; PR00423; CELLDVISETSZ.
TIGRPAMS; TIGR00065; ftsZ; 1.
PROSITE; PS01135; FTSZ 2; 1.
                                                                                                                                                                                                                                                                  Q9LDK5
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TRANSIT 1 31
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InterPro; IPR003008; Tubulin_FtsZ.
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    Physcomitrella patens (Moss)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 GCSAAEESKAMVEEALRGADMVFVTAGMGGGTGSGA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GTXXXXXSKQXEEEAVR-----LXXXXLXGGXSSGA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                          PRELIMINARY;
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47536 MW;
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                  PRT;
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Best Local S
Matches 12
                                                                                 C STRAINS-GSS1 / DSM 4299 / JCM 9571;

K MEDLINE-20570466; PubMed-11121031;

K MEDLINE-20570466; PubMed-11121031;

K Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

K Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,

K Kawashima T., Amano N., Koike H., Makino K., Suzuki M.;

Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

"Archaeal adaptation to higher temperatures revealed by genomic grant proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

R EMDL; AP000993; BAB59948.1; -.

R EMDL; AP000993; BAB59948.1; -.

R EMDL; AP000993; BAB59948.1; -.

R InterPro; IPR003008; Tubulin_FtsZ.

PRINTS; PR00993; tubulin_C. 1.

PRAM; PF03993; tubulin_C; 1.

R Pfam; PF03953; tubulin_C; 1.

R FINTS; PR00423; CELLDVISFTSZ.

R TIGREAMS; TIGR00065; ftsZ; 1.
               Best
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Pfam; PF00953; tubulin C; 1.
Pfam; PF009423; CELLDVISFTSZ.
PRINTS; PR00423; CELLDVISFTSZ.
TICRFAMS; TIGR00065; ftsZ; 1.
PROSITE; PS01135; FTSZ_2; 1.
PROSITE; PS000227; TUBULIN; 1.
                            Query Match
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Q97AK4;
01-OCT-2001 (TrEMBLrel. 1
01-OCT-2001 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indispensable for plastid division.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249140; CAB76387.1; ...
EMBL; AJ249139; CAB76386.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
NCBI_TaxID=3218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both their encoded proteins are importedinto chloroplasts and both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP-binding; Transit peptide.
TRANSIT 1 39
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                                                                                                                                                                                                                                                                                                                                                                                                      TV0806 OR TVG0806423.
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InterPro; IPR003008; Tubulin_FtsZ
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                                                                                                                                                                                                                                                                                                                                                           Thermoplasmataceae;
                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Thermoplasmata;
                                                                                                                                                                                                                                                                                                                                                                                        Thermoplasma volcanium.
                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=50339;
                                                                       Complete proteome.
               Local
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12; Conserv
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Similarity
8; Conserv
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                                                           347 AA;
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                                                                                                                                                                                                                                                                                                                                                               Thermoplasma.
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                                                            37421 MW;
               35.7%;
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Last annotation update)
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Pred. No. 18
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; 8D6659C5D2D6C0D3 CRC64;
   4.
               Score 40; DB
Pred. No. 17;
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                                                            5CC382D1BFA82331 CRC64;
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      Migmatches
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                               DB 17;
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                                 Length 347;
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ATU2765 OR AGR_C_5013.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Clelo C., Slater S.;

"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
                                                01-OCT-2001 (TrEMBLrel. 18, Creat ol-OCT-2001 (TrEMBLrel. 18, Last ol-OCT-2001 (TrEMBLrel. 18, Last Transcriptional factor regulator MLR3857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE009224; AAL43746.1; -. EMBL; AE008190; AAK88480.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003711; CarD.
Pfam; PF02559; TF_CarD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [CBI_TaxID=176299;
Bacteria; Proteobacteria;
                            Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                              Q98FB1;
                                                                                                                                                                                                                                       Q98FB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
                                                                                                                                                                                                                                                                                                                                                                                               154 NKMSETEAVRLVEVNLAKGPKRG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKOXEEEAVRLXXXXLXGGXSSG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21150 MW;
   Alphaproteobacteria; Rhizobiales;
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                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DE
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          785D4F2AA10A3DC4 CRC64;
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                                                                                                                                                                                                                                                 193 AA.
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Best Local :
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Q9RD53;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Matanabe A., Ideeawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP003002: BAB50656.1;
InterPro; IPR003711; CarD.
Pfam; PF02559; TF CarD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                               MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Ret of cordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomycineae; Streptomycetaceae; NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SC00629 OR SCF56.13C
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Cronin A., Fraser A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
Cerdeno A.M., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy L., Harris D.;
Submitted (DEC-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                 STRAIN=A3(2)
                                                                                                                                                   STRAIN=A3(2)
                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AA;
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e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53B7FFCCE907B538 CRC64;
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RESULT 8
Q9C812
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X MEDLINE-21016719; PubMed-11130712;

X MEDLINE-21016719; PubMed-11130712;

X MEDLINE-21016719; PubMed-11130712;

X MEDLINE-21016719; PubMed-11130712;

X Mitte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

X Mitte O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

X Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

X Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

X Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

X Chung M.K., Conn L., Conway A.B., Conway A.R., Fujii C.Y.,

X A. Langin-Hoper S., Johnson-Hopson C., Khan S., Khaykin E.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Liu X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Liu X.A., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Liu X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper S., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

X A. Langin-Hooper 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model coelicolor A3(2)";
Nature 417:141-147(2002).
Nature 417:141-147(2002).
EMBL; AL939.06; CAB62758.1; -...
HSSP; P03023; ILCC:
InterPro; IPR00193; Mitoch_carrier.
InterPro; IPR00193; Mitoch_carrier.
InterPro; IPR00193; Mitoch_carrier.
InterPro; IPR001761; PeriplaBP_Lac1.
Pfam; PF00523; PeriplaBP_lke; 1.
SMART; SM00354; HTH_LACC; 1.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Query Match
                                                                                    Nature 408:816-820(2000).

RATURE 408:816-820(2000).

EMBL; ACO51630; AAGS1222.1;

InterPro; IPRO02089; PPTA.

InterPro; IPRO01214; SET.

InterPro; IPRO01440; TPR.

Pfam; PF00515; TPR; 4.

SMART; SM00028; TPR; 3.

PROSITE; PS00904; PPTA; 1.

PROSITE; PS00904; PPTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat)
Hypothetical 87.1 kDa protein.
F10C21.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome 
SEQUENCE 369 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                              Hypothetical protein SEQUENCE 781 AA;
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8; Conserv
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                                                   87145 MW; F27B02CA82C35C76 CRC64;
     34.8%;
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Pred No. 28;
     Score 39;
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     DB
       10;
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     Length 781;
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RESULT 9
Q95DV5
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Best Local :
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Q95DV5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ311847; CAC44757.1; ...
InterPro; IPR000158; FtsZ.
InterPro; IPR00308; Tubulin_FtsZ.
Pfam; PF00391; tubulin; 1.
Pfam; PF03953; tubulin C; 1.
PRINTS; PR00423; CELLDVISFSZ.
PRINTS; PR00423; CELLDVISFSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum (Common tobacco). Chloroplast.
                                                                                                                                                                                                            Q9M436;
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Falconet D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FtsZ-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO0065; ftsZ; 1. PROSITE; PS01135; FTSZ_2; 1. GTP-binding; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thesis (2000), Department of Biological Sciences, University of Grenoble, Grenoble, France.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
El-Shami M., Alcaraz J.P., Lerbs-Mache S., Falconet D.; "A new cDNA encoding FtsZ-like protein from Nicotiana tabacum."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             El Shami M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV.
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                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana
                                                                                                              Nicotiana tabacum (Common tobacco)
Eukaryota; Viridiplantae; Streptop
                                                                                                                                                       Chloroplast FtsZ-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                         SEQUENCE FROM N.A
                                                                    NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 EMVKLASIQLASGDSSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                             176 GMNAANESKOAIEEAVYGADMVFVTAGMGGGTGTGA
                                                                                                                                                                                                                                                                                                                                                   l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                        4 GTXXXXXSKQXEEEAVR----LXXXXLXGGXSSGA
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                                                                                                                                                                                                                                                                                                                                                                                                            468 AA;
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                                                                                                                                                                  (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                             49174 MW;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    Score 38.5;
Pred. No. 4
                                                                                                                                                                                                                               PRT;
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                                                                                                               Embryophyta; Tracheophyta;
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                                                                                                   core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                 Length 468;
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RESULT 11
Q9JLY9
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                                                                                                   A Chiariotti L., Fedele M.;
A Chiariotti L., Fedele M.;
I Submitted (JAN 1999) to the EMBL/GenBank/DDBJ databases.

EMBL; ART19255; AART2517.1; -.

R MGD; MGI:1891832; Zfp278.

R InterPro; IPR000637; AT book.

R InterPro; IPR007087; ZnF C2H2.

Pfam; PF02178; AT_book; I.

Pfam; PF02178; AT_book; I.

SWART; SM00355; ZnF C2H2; I.

DR SWART; SM00355; ZnF C2H2; I.

DR SMART; SM00354; HWGI_Y; I.
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Matches 12
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01-OCT-2000
01-MAR-2003
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Pfam; PF03953; tubulin C; 1.
PRINTS; PR00423; CELLDVISTSZ.
TIGREAMS; TIGR00065; ftsZ; 1.
PROSTIE; PS01135; FTSZ 2; 1.
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GTP-binding
                                                                                                                                  PROSITE; PS00354; HMGIY; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS00157; ZINC_FINGER_C2H2_2; 1.

Metal_binding; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20179892; PubMed=10713105;
Fedele M., Benvenuto G., Pero R., Majello B.
Vollono E., Day P.M., Santoro M., Lania L.,
                                                                                                                                                                                                                                                                                                                                                                                Chiatiotti L.;
"A novel member of the BTB/POZ family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATZ (Fragment).
ZFP278 OR PATZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JLY9;
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                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 12; Conser
                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                                                                                                                                                                                                                                                                                                                      finger protein and acts as a transcriptional repressor.";
col. Chem. 275:7894-7901(2000).
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N
                                               Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMNAANESKQAIEEAVYGADMVFVTAGMGGGTGTGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTXXXXXSKQXEEEAVR----LXXXXLXGGXSSGA 34
                        SKOXEEEAVRLXXXXLXGGXS 31
 SMOPEEEAARATGAAIAGQAS
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(TrEMBLrel.)
                                                                                                   163 AA;
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                                                Conservative
                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                               163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                   17227 MW; 60A3046938B4FC9D CRC64;
                                                             33.9%;
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Last annotation update)
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                                                Score 38; DB Pred. No. 18; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred. No. 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                          Majello B., Battista S., Lembo F., Lania L., Bruni C.B., Fusco A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA
                                                                                                                                                                                                                                                                                                                                                                                PATZ, associates with the RNF4
                                                                         DB 11; Length 163;
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RESULT 12
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070379
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 070379; PRELIMINARY; PRT; 289 AA. 070379; 01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-AUG-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
"Purification, molecular cloning, and characterization of TRP32, novel thioredoxin-related mammalian protein of 32 kDa.";
J. Biol. Chem. 273:19160-19166(1998).
EMBL; AF052660; AAC40183.1; -.
HSSP; 043396; 1GH2.
MSD; MGI:1860078; Txnl.
InterPro; IPR006663; Thiored.
InterPro; IPR006663; Thiored.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus CBI_TaxID=10090;
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HSSP; P29995; IAIS.
InterPro; IPR006670; Cyclin.
InterPro; IPR000812; TFIIB euk.
Pfam; PF00382; transcript fac2;
PRINTS; PR00685; TIFACTORTIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0685; TIFACTOR: SMART; SM00385; CYCLIN; 2 PROSITE; PS00782; TFIIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus horikoshii.
                                                                                                                                                                                                                            Lee K.K., Murakawa M., Ta
Sakamaki K., Yonehara S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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36.4%;
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07, Last sequence update)
23, Last annotation update)
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Pred. No. 24;
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Ohfuku Y.,
N., Oguchi A.,
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RESULT
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Q8XCN1
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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PROSITE; PS00194; THIOREDOXIN;
SEQUENCE 289 AA; 32251 MW;
                                                                                                                 STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; X81461; CAD30711.1; -. SEQUENCE 310 AA; 34486 MW; 54AA2C8C6507FFEE CRC64;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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SEQUENCE FROM N.A. STRAIN=0157:H7 / F
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Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                        Nature 409:529-533(2001).
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                                                                                                 "Genome sequence of enterohaemorrhagic
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Pred. No. 37;
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                             Q8ZNA4;
Q8ZNA4;
01-MAR-2002
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                                                                                                    YFDC OR STM2393.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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EMBL, AE016764; AAN81342.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 310 AA; 34524 MW; A7AD75C3AA31EFBF CRC64;
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Enterobacteriaceae; Escherichia.
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Hypothetical protein yfdC.
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MEDLINE=22388234; PubMed=12471157;
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01-MAR-2002 (TrEMBLrel.
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                                                               Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                              Putative transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38;
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PRESENTE SECURE OF MESSAGE AND SECURE OF MES
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BACAGO
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Best Local S
Matches 8
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TO "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
RMBL, AL627274; CAD07625.1; -
EMBL, AL627274; CAD07625.1; -
SMBUL, AL627274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                               01-DEC-2001
01-DEC-2001
01-OCT-2002
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"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE008807; AALCACOTO.;
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
SEQUENCE 313 AA; 34917 MW; 430A474E07B640AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                   Q94D21;
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   P0025A05
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nes 8; Conserv
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                               KOXEEEAVRLXXXXXXGGXSSGA 34
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protein
                                   (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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Pred. No. 38;
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RESULT 20
Q9HD72
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Best Local
                                                         Matches
                                                                                                               Pfam; pF02178; AT hook; 1.

Pfam; pF00251; BTB; 1.

Pfam; pF00055; BTB; 1.

SMART; SM00384; AT hook; 1.

SMART; SM00325; BTB; 1.

SMART; SM00325; BTB; 1.

SMART; SM00325; BTB; 1.

PROSITE; pS00402; BPD TRANSP_INN_MEMBR; 1.

PROSITE; pS00402; BTB; 1.

PROSITE; pS00354; HMGI Y; 1.

PROSITE; PS00354; HMGI Y; 1.

PROSITE; PS0028; ZINC_FINGER_C2H2_1; 3.

PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ BWBL; AF24252; AAF99602.1; -. HSSP; Q05516; 1CS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Krueppel-related zinc finger protein SBZF5.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; Q94D21; -. SEQUENCE 317 AA;
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Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                             InterPro; IPR000637; AT hook.
InterPro; IPR000515; BPD transp.
InterPro; IPR0005210; BTB_POZ.
InterPro; IPR007087; Znf CZH2.
Pfam; PF02178; AT_hook; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9HD72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HD72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 EANEEALALLIDYLSSGNSPGA 184
205
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                                                                        Similarity
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 SMQPEEEAARAAGAA I AGQAS
                            SKOXEEEAVRLXXXXLXGGXS 31
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                                                          Conservative
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                                                                       33.9%;
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                                                         <del>--</del>
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                                                                       Score 38; DB
Pred. No. 53;
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                                                            Mismatches
                                                                                                                     6B3CCDA886941F20 CRC64;
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                                                                                       4; Length 424;
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Quintero V., Cevallos M.A., Davila G.;

"A site-specific recombinase and RecA are required to exert
incompatibility towards the symbiotic plasmid of Rhizobium etl
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

R EMBL; U80928; AAM54801.1; -.

R InterFro; IPR001128; Cytochrome_P450.

R Pfam; PF00067; p450; 1.

R PRINTS; PR00385; P450.

R PRINTS; PR00385; P450.

R PROSITE; PS00086; CYTOCHROME P450; 1.

R PGOSITE; PS00086; CYTOCHROME P450; 1.
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Q8KLD9;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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Bacteria; Proteobacteria;
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"Sequence, localization and characteristics of the replicator region of the symbiotic plasmid of Rhizobium etli.";
Microbiology 143:2825-2831(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HBE3;
Q9HBE3;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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ZSG.
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   MEDLINE=20404868; PubMed=10949935;
Mastrangelo T., Modena P., Tornielli S., Bullrich F., Testi A.,
Mezzelani A., Radice P., Azzarelli A., Pilotti S., Croce C.,
Pierotti M., Sozzi G.;
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9606;
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nes 9; Conserv
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03 (TrEMBLrel.
e p450, CpxP2.
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                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
(TremBlrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                           Chordata;
Primates;
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Last annotation update)
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Pred. No. 53;
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                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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plasmid
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smid of Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Indels
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Q9HBE2
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Pfam; PF002178; AT hook: 1.

Pfam; PF002178; AT hook: 1.

Pfam; PF00056; Eff2H2; 4.

ProDom; PD000003; Znf C2H2; 1.

SMART; SM00384; AT hook; 1.

SMART; SM00325; BTB; 1.

SMART; SM00325; BTB; 1.

SMART; SM00355; ZnF C2H2; 4.

PROSITE; PS00402; BPD TRANSP_INN_MEMBR; 1.

PROSITE; PS00402; BPD TRANSP_INN_MEMBR; 1.

PROSITE; PS00354; BPD TRANSP_INN_MEMBR; 1.

PROSITE; PS00028; ZNC_FINGER_C2H2_1; 4.

PROSITE; PS00028; ZNC_FINGER_C2H2_1; 4.
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Best Local
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Q9HBE2;
01-MAR-2001
01-MAR-2001
01-MAR-2003
Zinc finger i
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EMBL; BC021091; AAH21091.1; -.
HSSF; Q05516; 1CS3.
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Oncogene 19:3799-3804(2000).
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InterPro; IPR000515; BPD_transp.
InterPro; IPR000210; BTB_PCZ.
InterPro; IPR007087; Znf_C2H2.
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Pfam; PF02178; AT hook; I.

Pfam; PF00551; BTB; I.

Pfam; PF00096; Zf-C2H2; 6.

PrcDom; PD000003; Znf_C2H2; 1.

SMART; SM00384; AT hook; 1.

SMART; SM00325; BTB; I.

SMART; SM00355; Znf_C2H2; 6.

PROSITE; PS00402; BFD_TRANSP_INN_MEMBR; 1.
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                          EMBL; AF254084; AAG09033.1; -.
HSSP; Q05516; ICS3.
InterPro; IPR000637; AT hook.
InterPro; IPR000515; BPD transp.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR007087; Znf_C2H2.
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Mastrangelo T., Modena P., Tornielli S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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(TrEMBLrel. 16, Last sequence up)
(TrEMBLrel. 23, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10949935;
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vi
Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bullrich F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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RESULT
Q9P1A9
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RESULT 25
                                                                                                                                                                                 Best Loc
Matches
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HSSP, Q05516; 1C33.
INTERPRO; IPR000637; AT hook.
InterPro; IPR000515; BPD_transp.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR000787; Znf_C2H2.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF02178; AT hook; 1.
Pfam; PF00051; BTB; 1.
R Pfam; PF00096; Zf-C2H2; 4.
R Pfam; PF00096; Zf-C2H2; 1.
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Best Local
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                                                                                                                                                                                                                                                                                                    SWART; SM00384; AT hook; 1.

SWART; SM00385; BTB; 1.

SWART; SM00355; ZBP C2H2; 4.

SWART; SM00355; ZBP TRANSP INN_MEMBR; 1.

PROSITE; PS0097; BTB; 1.

PROSITE; PS000354; HMGI Y; 1.

PROSITE; PS000384; HMGI Y; 1.

PROSITE; PS00138; ZINC_FINGER_C2H2_1; 4.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

Metal-binding; Zinc; Zinc; TA4440724C947
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01-OCT-2000
01-OCT-2000
01-MAR-2003
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PROSITE; PS00354; HWGI Y; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.

Metal-binding; Zinc; Zinc-finger:

Metal-binding; Zinc-finger:

Metal-bindi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiariotti L., Fedele M.; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF119256; AAF32518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chiatiotti L.;
"A novel member of the BTB/POZ family, PATZ, associates with the RNF4 RING finger protein and acts as a transcriptional repressor.";
J. Biol. Chem. 275:7894-7901(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20179892; PubMed=10713105;
Fedele M., Benvenuto G., Pero R., Majello B., Battista S., Lembo F.,
Vollono E., Day P.M., Santoro M., Lania L., Bruni C.B., Fusco A.,
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SECUENCE 537 AA;
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9; Conserv
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9; Conservative
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Pred. No.
                                                                                                                                                                                                           Score 38; DB
Pred. No. 68;
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RESULT 26
Q8RM05
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Best Local S
Matches 9
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## Pfam; PF00696; zf-C2H2; 7.

## PF00096; zf-C2H2; 1.

## PF0Dom; PD000003; Znf C2H2; 1.

## SMART; SM00384; AT hook; 1.

## SMART; SM00325; BTB; 1.

## SMART; SM00325; Znf C2H2; 7.

## PROSITE; PS00402; BFD TRANSP_INN_MEMBR; 1.

## PROSITE; PS00402; BTB; 1.

## PROSITE; PS00324; HMGI Y; 1.

## PROSITE; PS00324; HMGI Y; 1.

## PROSITE; PS00328; ZINC_FINGER_C2H2_1; 6.

## PROSITE; PS00328; ZINC_FINGER_C2H2_2; 6.

## Hypothetical protein; Metal-binding; Zinc-finger.

## SEQUENCE 616 AA; 66319 MW; EEECEODIF92B8010 CRC64;
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Q9Y529;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human)
                                                                           Ensign S.A.;
"Blochemical, Molecular and Genetic Analyses of the Acetone "Blochemical, Molecular and Genetic Analyses of the Acetone Capsulatus strain B10.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-UTN-2002 (TrEMBLrel. 21, Created
01-UTN-2002 (TrEMBLrel. 21, Last at
01-MAR-2003 (TrEMBLrel. 23, Last at
Sigma-54 dependent transcriptional
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InterPro; IPR000515; BPD transp.
InterPro; IPR000510; BTB POZ.
InterPro; IPR007087; Znf C2H2.
Pfam; PF02178; AT hook; 1.
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EMBL; AY055852; AAL17709.1; -.
InterPro; IPRO03593; AAA_ATPase
InterPro; IPRO0318; GAF.
InterPro; IPR002197; HTH_Fis.
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                                                                                                                                                                  STRAIN=Py2;
Sluis M.K., Larsen R.A., Krum J.G., Anderson R., Metcalf W.W.,
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                               Xanthobacter sp. (strain Py2).
                                                                            -1- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
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nes 9; Conservat
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JUL-1999) to the
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Last annotation update)
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RESULT 27
Q9UDU0
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Pfam; PF00158; Sigma54_activat; 1.

SMART; SM00302; AAA; 1.

SMART; SM00065; GAF; 1.

TIGREAMS; TIGR01199; HTH fis; 1.

PROSITE; PS00675; SIGMA54_INTERACT_1; 1.

PROSITE; PS00688; SIGMA54_INTERACT_4; 1.

PROSITE; PS0045; SIGMA54_INTERACT_4; 1.

PROSITE; PS00048; SIGMA54_INTERACT_4; 1.

PROSITE; PS00048; SIGMA54_INTERACT_4; 1.

PROSITE; PS00045; SIGMA54_INTERACT_4; 1.
            SEQUENCE FROM N.A.

Chin K.-V., Yang W.-L., Kudoh K.;

Chin K.-V., Yang W.-L., Kudoh K.;

Chin K.-V., Yang W.-L., Kudoh K.;

Nivel cAMP Signalling Via the Regulatory Subunit of the dependent Protein Kinase.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AC005003; AAF01349.1; -.

EMBL; APC24083; AAF019024.1; -.

EMBL; AY028384; AAK19024.1; -.

HSSP; Q05516; 1CS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99063792; PubMed=9847074;
Sulston J.E., Waterston R.;
"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
WUGSC:H DJ400N23.1 protein (Zinc finger sarcoma gene long A isoform)
(BTB-POZ domain zinc finger transcription factor).
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Mastrangelo T., Modena P., Tornielli S., Bullrich F., Tes
Mezzelani A., Radice P., Azzarelli A., Pilotti S., Croce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      Mezzelani A., Radice P., Azzarelli A., Pilotti S., Croce C., Pierotti M., Sozzi G.; Pierotti M., Sozzi G.; Pierotti M., Sozzi G.; Pierot is fused to EWS in small round cell tumor."; "A novel zinc finger gene is fused to EWS in small round cell tumor."; Oncogene 19:3799-3804(2000).
                                                                                                                                                                                                                                                                                                                            Waterston R.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1998) to the
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TRANSFAC; T04797; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geisel C., Murray J.;
.ce of Homo sapiens PAC clone RP3-400N23.";
JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 82;
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Best Local S
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SMART; SM00384; AT hook; 1.

SMART; SM00385; Znf C2H2; 7.

SMART; SM00355; Znf C2H2; 7.

PROSITE; PS004402; BPD TRANSP_INN_MEMBR; 1.

PROSITE; PS00097; BTB; 1.

PROSITE; PS00097; BTB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 6.
                        Pfam; PF00096; zf-C2H2; 7.

PF0Dom; PF000003; Znf C2H2; 1.

SMART; SM00384; AT hook; 1.

SMART; SM00385; ZnF C2H2; 7.

PROSITE; PS00402; BPD TRANSP INN_MEMBR; 1.

PROSITE; PS00402; BPD TRANSP INN_MEMBR; 1.

PROSITE; PS00384; HWGI Y; 1.

PROSITE; PS00384; HWGI Y; 1.

PROSITE; PS00384; HWGI Y; 1.

PROSITE; PS00384; TNC_FINGER_C2H2_1; 6.

PROSITE; PS00187; ZINC_FINGER_C2H2_2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                        domain.";

Mol. Cell. Biol. 20:1733-1

EMBL; AB022397; BAA90874.1

HSSP; Q05516; 1CS3.

TRANSFAC; T04796; -

MGD; MGI:1891832; Zfp278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9JMG9
Q9JMG9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02178; AT hook; 1.
Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C2H2; 7.
ProDom; PD000003; Znf_C2H2; 1.
                                                                                                                                                                                                                                                                                                                                          MEDLINE=20136053; PubMed=10669750; Kobayashi A., Yamagiwa H., Hoshino H., Muto A., Sato K., Morita M., Hayashi N., Yamamoto M., Igarashi K.; Hayashi N., Yamamoto M., Igarashi K.; "A combinatorial code for gene expression generated by transcription factor bach2 and MAZR (MAZ-related factor) through the BTB/POZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metal-binding; Zinc; Zinc-ring
SEOUENCE 641 AA; 69079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000210;
InterPro; IPR007087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription factor MAZR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
    Metal-binding;
SEQUENCE 641
                                                                                                                                                                     Pfam; PF02178; AT hook; 1. Pfam; PF00651; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZFP278 OR MAZR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                 InterPro; IPR000637; AT hook.
InterPro; IPR000515; BPD transp.
InterPro; IPR000210; BTB POZ.
InterPro; IPR007087; Znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 SKOXEEEAVRLXXXXLXGGXS 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMOPEEEAARAAGAAIAGQAS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000637; AT_hook.
IPR000515; BPD_transp.
IPR000210; BTB_POZ.
IPR007087; Znf_C2H2.
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9397; BAA90874.1; -.
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zinc;
AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%;
   ; Zinc-finger.
69138 MW; C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29515535E380F0CE CRC64;
       C4BEA972CC15A877 CRC64;
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RESULT 30
Q8XZE
ID C9XZE
AC Q9XZE
AC Q9XZE
AC Q9XZE
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DE PUTAL
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Best Local S
Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q05516; 1CS3.
Genew; HGNC:13071; ZNF278.
InterPro; IPR000637; AT hook.
InterPro; IPR000637; BTD transp.
InterPro; IPR000515; BPD transp.
InterPro; IPR000210; BTB POZ.
InterPro; IPR007087; Znff C2H2.
Pfam; PF002178; AT hook; I.
Pfam; PF002178; AT hook; I.
Pfam; PF00096; Zff-C2H2; 1.
Pfam; PF00096; Zff-C2H2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=20404868; PubMed=10949935;

Mastrangelo T., Modena P., Tornielli S., Bullrich F., Testi

Mezzelani A., Radice P., Azzarelli A., Pilotti S., Croce C.,

Mezzelani A., Sozzi G.;

Pierotti M., Sozzi G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9HBB1;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
     QBXZE5;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative betaine aldehyde dehydrogenase (BADH) oxidoreductase
(EC 1.2.1.8)
8ETB OR RSC1456 OR RS03851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                           SMART; SM00284; AT hook; 1.

SMART; SM00225; BTB; 1.

SMART; SM00325; BTB; 1.

SMART; SM00355; ATF C2H2; 8.

PROSITE; PS00402; BFD_TRANSP_INN_MEMBR; 1.

PROSITE; PS00402; BFD_TRANSP_INN_MEMBR; 1.

PROSITE; PS00324; HMGI Y; 1.

PROSITE; PS00328; ZINC_FINGER_C2H2_1; 7.

PROSITE; PS00328; ZINC_FINGER_C2H2_2; 7.

Metal_binding; Zinc; ZINC_FINGER_C2H2_2; 7.

Metal_binding; Zinc; ZINC_FINGER_C2H2_2; 7.

Metal_binding; Zinc; ZINC_FINGER_C2H2_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A novel zinc finger gene is fused to EWS in small round cell tumor."; Oncogene 19:3799-3804(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc finger sarcoma gene long C isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9HBE1
                                                                                                                                     Q8XZE5
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Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 SMOPEEEAARATGAAIAGQAS 225
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                                                                                                                                                                                                                                                                                         Similarity 42.9%; Score 38; DE Similarity 42.9%; Pred. No. 90; 9; Conservative
                                                                                                                                                                                                                                                         SKOXEEEAVRLXXXXLXGGXS 31
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                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.9%; Score 38;
42.9%; Pred. No.
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                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                        478 AA.
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                                                                    Matches
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Best Local S
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Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Chandler M., Choisne N., Claudel-Renard C., Saurin W., Schiex T.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415,497-502(2002).
                                                                                                                                                                     MAGULE #13-19 ( DAZINO)

EMBL; AL64064; CAD15.158.1; .

InterPro; IPR002086; Aldehyde_dehydr.

Pfam; PP00171; aldedh; 1.

PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.

PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                     Oxidoreductase; Complete proteome. SEQUENCE 478 AA; 50375 MW; F1!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=305;
 393 ÉÉÉAIRIANDSIYGLAGGVWSG 414
                                 15 EEEAVRLXXXX---LXGGXSSG 33
                                                                                     Similarity
                                                                  Conservative
                                                                                 33.5%;
45.5%;
                                                                      <u>۲.</u>
                                                                                       Score 37.5;
Pred. No. 76
                                                                                                                                         F1ADA761C20CDC1A CRC64;
                                                                      Mismatches
                                                                                                         DB 16;
                                                                        7:
                                                                                                        Length 478;
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Search completed: December 23, 2003, 10:03:52 Job time : 31.5 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
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Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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Gapop 10.0 , Gapext 0.5
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298.814 Million cell updates/sec
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112
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Listing first 50 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	* Query Match Length	B 0	ID	Description
1	70.5	62.9	36	10	US-09-003-869-171	Sequence 171, App
N	70.5	2	36	11	US-09-756-690A-171	Sequence 171, App
w	70.5		36	15	US-10-157-224A-171	•
4	70.5		36	15	US-10-187-051-171	171,
U	70.5		37	10	บร-09-003-869-99	99,
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7	70.5	•	37	11	US-09-756-690A-99	Sequence 99, Appl
œ	70.5		37	11	US-09-756-690A-183	
9	70.5		37	15	US-10-157-224A-99	Sequence 99, Appl
10	70.5		37	15	US-10-157-224A-183	
11	70.5		37	15	US-10-187-051-99	Sequence 99, Appl
12	70.5	62.9	37	15	US-10-187-051-183	Sequence 183, App
13	70.5		39	10	US-09-003-869-35	Sequence 35, Appl
14	70.5		39	10	US-09-003-869-36	Sequence 36, Appl
15	70.5		39	10	US-09-003-869-39	Sequence 39, Appl

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-09-003-869-6	-TU-18/-U51-18-	10-187-051-1	-10-187-051-86	-10-18/-051-b	S-10-157-224A-18	-10-157-224A-1	S-10-157-224A-86	S-10-157-224A-6	-09-756-690A-18	-09-756-690A-1	-09-756-690A-86	-09-756-690A-6	-09-003-869-18	-09-003-869-17	-09-003-869-86	-09-003-869-6	-10-187-051-1	-10-187-051-69	-10-157-224A-1	-10-157-224A-69	-09-756-690A-1	-09-756-690A-69	-09-003-869-1	-09-003-869-69	-09-756-690A-	-10-187-051-39	-10-187-051-3	-10-187-051-3	-10-157-224A-3	-10-157-224A-3	-10-157-224A-3	-09-756-690A-3	9-756-690A	- (9- /56-690A-5	00 756 6003-3
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ALIGNMENTS

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US-09-003-869-171

US-09-003-869-171

Sequence 171, Application US/09003869A

Patcht No. US20020137666A1

PATCH INFORMATION:

APPLICANT: BEELEY, NIGEL ROBERT ARNOLD

APPLICANT: HEAVSAR, SUMIL

ITILE OF INVENTION: THE REDUCTION OF FOOD INTAKE

FILE REFERENCE: 231/181

CURRENT FILING DATE: 1997-01-07

EARLIER REPLICATION NUMBER: US 60/034,905

EARLIER REPLICATION NUMBER: US 60/055,404

EARLIER REPLICATION NUMBER: US 60/055,404

EARLIER REPLICATION NUMBER: US 60/065,442

EARLIER REPLICATION NUMBER: US 60/065,442

EARLIER REPLICATION NUMBER: US 60/066,029

EARLIER FILING DATE: 1997-11-14

INMUSER OF SEQ ID NOS: 188

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 171

LENGTH: 36

TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE
OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist
OTHER INFORMATION: compound
FEATURE: AMIDATION
UCCATION: (36)...(36)
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                                                                                    CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1990-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver. 2.1
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CURRENT EPLING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/175,365

PRIOR FILING DATE: 2000-01-10

NUMBER OF SEQ ID NOS: 188

SOPTWARE: PATENTIN Ver 2.1

SEQ ID NO 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 171, Applic Publication No. US20 GENERAL INFORMATION:
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                                                               SEQ ID NO 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOLTERMAN, ORVILLE G. APPLICANT: YOUNG, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 0201-050
FILE REFERENCE: 0201-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: amidated Pro (Prolinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: c-term amidation
ORGANISM: Artificial Sequence
                                          ENGTH:
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Local Similarity 59.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%; Score 70.5; DB 11
Local Similarity 59.4%; Pred. No. 5.8e-06;
Les 19; Conservative 0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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Pred. No. 5.8e-06;
0; Mismatches 12;
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CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR PILING DATE: 1997-08-08
PRIOR PILING DATE: 1997-08-08
PRIOR PILING DATE: 1997-08-08
PRIOR PILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
PRIOR PRIOR DATE: 1997-11-14
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US-10-187-051-171
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                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                          Sequence 99, Application US/09003869A; Patent No. US20020137666A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THERBOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 231/181
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OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: artificially synthesized sequence of novel exendin
OTHER INFORMATION: agonist
OTHER INFORMATION: compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (36)...(36)
OTHER INFORMATION: amidated Pro (Prolinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: AMIDATION LOCATION: (36)...(36
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Local Similarity 59.4%; Pred. No. 5.8e-06
Les 19; Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.9%;
Similarity 59.4%;
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Pred. No. 5.8e-06;
0; Mismatches 12;
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EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 99
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BESLEY, NIGEL ROBERT ARNOLD
APPLICANT: BESLEY, NIGEL ROBERT ARNOLD
APPLICANT: BHAVSAR, SUNIL
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE OF INVENTION: THE REDUCTION OF FOOD INTAKE
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT APPLICATION NUMBER: US 60/034,905
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER APPLICATION NUMBER: US 60/065,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEO ID NOS: 188
NUMBER OF SEO ID NOS: 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-003-869-99
                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/003,869A
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NAME/KEY: AMIDATION
LOCATION: (37)...(37)
OTHER INFORMATION: amidated Nmeala (n-methylalaninamide)
                                                                                                                                                                OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: amidated hPro (homoprolinamide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: AMIDATION LOCATION: (37)...(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                           OTHER INFORMATION: Xaa in positions 31,
                                                                                                                                        FEATURE
                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                      ENGTH:
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                                                                                                           and 37 stands for n-methylalanine
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RESULT 8
(US-09-756-690A-183)
(Sequence 183, Application US/09756690A)
(Sequence 183, Application US20030036504A1)
(Publication No. US20030036504A1)
(SENERAL INFORMATION:
(APPLICANT: YOUNG, ANDREW A.
APPLICANT: YOUNG, ANDREW A.
APPLICANT: YOUNG, ANDREW A.
FILE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
(FILE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
(FILE REFERENCE: 249/124
(CURRENT FILING DATE: 2002-04-19
(PRIOR APPLICATION NUMBER: 60/175,365
(PRIOR APPLICATION NUMBER: 60/175,365
(PRIOR FILING DATE: 2000-01-10
(NUMBER OF SEQ ID NOS: 188)
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Publication No. US20030036504A1
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CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver 2.1
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APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
FILE REFERENCE: 249/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (37)
OTHER INFORMATION: hPro
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20; Conservative
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Pred. No. 6e-06;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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US-10-157-224A-99
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR TILING DATE: 2000-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 99
LENGTH: 37
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD_RES
LOCATION: (37)
OTHER INFORMATION: NMeala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (36)
OTHER INFORMATION: NMeala
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NAME/KEY: MOD_RES
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                                                    REATURE:
NAME/KEY: MOD_RES
LOCATION: (36)..(37)
OTHER INFORMATION: Homoproline
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                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (31)
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                                                                                                                                    OTHER INFORMATION: Homoproline
                                                                                                                                                                                                             OTHER INFORMATION: c-term amidation
                                                                                                                                                                                                                                  FEATURE:
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  62.9%;
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Pred. No. 6e-06;
  Score 70.5;
  DB 15;
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Length 37;
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Sequence 99, Application US/10187051

Publication No. US20030087821A1

GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: PRICKETT, KATHRYN S.

ITILE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT PILLING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1900-01-01
PRIOR FILING DATE: 2000-01-01
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver. 2.1
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NAME/KEY: MOD_RES
LOCATION: (36)...(37)
OTHER INFORMATION: N-methylalanine
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ORGANISM: Artificial Sequence
PRIOR APPLICATION NUMBER: US 60/034,905
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OTHER INFORMATION: N-methylalanine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 62.9%; Score 70.5; DB 15; Similarity 62.5%; Pred. No. 6e-06; 20; Conservative 0; Mismatches 11;
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0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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US-10-187-051-183
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                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 183, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOI
APPLICANT: BRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 99
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR EILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
PRIOR FILING DATE: 1997-11-14
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APPLICANT: BHAVGAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: artificially synthesized sequence of novel exendin OTHER INFORMATION: agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: compound
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                                                                                                                                                                         OTHER INFORMATION: artificially synthesized sequence OTHER INFORMATION: agonist
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                                                                                                                                                      OTHER INFORMATION: compound
                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                            OTHER INFORMATION: Xaa in positions 31, 36 and 37 stands for n-OTHER INFORMATION: methylalanine.
                                                                                                                             FEATURE:
LOCATION: (37)...(37)
                        NAME/KEY: AMIDATION
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Pred. No. 66
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, OTHER INFORMATION: amidated Nmeala (n-methylalaninamide) US-10-187-051-183
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EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
                                                                                                                                                                                                                                                            US-09-003-869-36
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GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT ENLING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
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Matches 20; Conservative
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                                                                                                                                                                                                                Sequence 36, Application US/09003869A Patent No. US20020137666A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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CURRENT FILING DATE: 1998-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 231/181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                    4 GTFTSDLSKOLEBEAVRLFIEFLKNGGXSSGA 35
                                                                                                                                                                                                                                                                                                                                                                                            4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Pred. No. 6e
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Pred. No. 6.3e-06;
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EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER: OF SEQ ID NOS: 188
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
SEQ ID NO 36
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1996-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER REPLICATION NUMBER: US 60/055,404
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER REPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
NUMBER OF SEQ ID NOS: 188
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                                                                                  US-09-003-869-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09003869A Patent No. US20020137666A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 39
                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BEELEY, NIGEL ROBERT ARNOLD APPLICANT: PRICKETT, KATHRYN S. APPLICANT: BHAVSAR, SUNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: AMIDATION
LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                   LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
                                                                                                                                               FEATURE:
NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                     OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
                                                                                                                                                                                                                OTHER INFORMATION: Xaa in positions 31,
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Pred. No. 6.3e-06;
0; Mismatches 11;
     Score 70.5; DB 10;
Pred. No. 6.3e-06;
                                                                                                                                                                                                                      36,
                                                                                                                                                                                                                         37 and 38 stands for n-methylalanine
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US-09-756-690A-36
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                                                                                                                                                                                                                                       ; Sequence 36, Application US/09756690A ; Publication No. US20030036504A1 ; GENERAL INFORMATION:
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TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: KOLTENAN, ORVILLE G.
APPLICANT: KOLTENAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
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LOCATION: (31)
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LOCATION: (38)
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LOCATION: (37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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RESULT 18
US-09-756-690A-39
US-09-756-690A-39
Sequence 39, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver 2.1
SEQ ID NO 39
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                                                                                                                                             FEATURE:

NAME/KEY: MOD RES

NAME/KEY: MOD RES
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APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver 2.1
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OTHER INFORMATION: tPro
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LOCATION: (38)
OTHER INFORMATION: tPro
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OTHER INFORMATION: tPro
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NAME/KEY: MOD_RES
                                                  LOCATION: (37)
OTHER INFORMATION: MeAla
                                                                           NAME/KEY: MOD_RES
                                                                                                                                LOCATION: (36)
OTHER INFORMATION: MeAla
                                                                                                                                                                                                                OTHER INFORMATION: MeAla
                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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LOCATION: (37)
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LOCATION: (31)
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Pred. No. 6.3e-06;
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RESULT 20
US-10-157-224A-36
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OTHER INFORMATION: thioproline
US-10-157-224A-35
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; OTHER INFORMATION: c-term amidation US-09-756-690A-39
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CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR PILING DATE: 2000-01-10
NUMBER: 05/105,365
PRIOR FILING DATE: 2000-01-10
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Sequence 36, Application US/10157224A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: KOLTERMAN, ORVILLE G.
TITLE OF INVENTION: ANDEL EXENDIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 02001-050
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SEQ ID NO 35
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APPLICANT: KOLTERWAN, ORVILLE G.
APPLICANT: KOLTERWAN, ORVILLE G.
TITLE OF INVENTION: NOVEL EXEMBIN AGONIST FORMULATIONS AND METHODS OF
TITLE OF INVENTION: ADMINISTRATION THEREOF
FILE REFERENCE: 0.2001-0.50
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NAME/KEY: MOD RES
LOCATION: (31)
OTHER INFORMATION: thioproline
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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Local Similarity 62.5%;
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Local Similarity 62.5%;
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Pred. No. 6.3e-06;
0; Mismatches 11;
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CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/889,330
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 1999-01-14
PRIOR FILING DATE: 2000-01-10
NUMBER: 06/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER: 07 SEQ. ID NOS: 188
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/00902
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
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SEQ ID NO 36
LENGTH: 39
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                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL EXENDIN AGONIST FORMULATIONS AND METHODS OF TITLE OF INVENTION: ADMINISTRATION THEREOF FILE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2002-05-28
CURRENT FILING DATE: 2002-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: YOUNG, AND APPLICANT: KOLTERMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: homoproline
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LOCATION: (36)..(
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OTHER INFORMATION: homoproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                             FEATURE: OTHER INFORMATION: c-term amidation
                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: N-methylalanine
                                            NAME/KEY: MOD_RES
                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist
                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GTFTSDLSKOLEEBAVRLFIEFLKNGGXSSGA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 39;
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APPLICANT: PRICKETT, KATHRYN S.

APPLICANT: BHAVGAR, SUNIL

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR

TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE

FILE REFERENCE: 231/181

CURRENT APPLICATION NUMBER: US/10/187,051

CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US/09/003,869

PRIOR APPLICATION NUMBER: US/09/003,905

PRIOR APPLICATION NUMBER: US 60/034,905

PRIOR FILING DATE: 1997-01-07

PRIOR APPLICATION NUMBER: US 60/055,404

PRIOR FILING DATE: 1997-08-08

PRIOR APPLICATION NUMBER: US 60/055,404

PRIOR APPLICATION NUMBER: US 60/056,402

PRIOR APPLICATION NUMBER: US 60/066,029

PRIOR APPLICATION NUMBER: US 60/066,029

PRIOR APPLICATION NUMBER: US 60/066,029

PRIOR PILING DATE: 1997-11-14
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US-10-187-051-35
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                                                                                                                                                                                                                                                                                            ; NAME/KEY: AMIDATION
; LOCATION: (39)...(39)
; OTHER INFORMATION: amidated Ser (Serinamide)
US-10-187-051-35
RESULT 23
US-10-187-051-36
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Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
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Best Local (
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NAME/KEY: MOD_RES
LOCATION: (36)...(38)
OTHER INFORMATION: N-methylalanine
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                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa in positions 31, 36, 37 and 38 stands for OTHER INFORMATION: thioproline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: artificially synthesized sequence of novel exendin OTHER INFORMATION: agonist OTHER INFORMATION: compound
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ORGANISM: Artificial Sequence
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                                                                                                                                               4 GTXXXXXXXXXXXEEEAVRLXXXXL-XGGXSSGA 34
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                                                                                                   GTFTSDLSKQLEEEAVRLFIEFLKNGGXSSGA 35
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Sequence 36, Application US/10187051
Publication No. US20030087821A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.

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                                                NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 39
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Publication No. US20030087821A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36
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PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
PRIOR FILING DATE: 1997-11-14
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CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
PRIOR FILING DATE: 1997-01-07
                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/055,404
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: US 60/065,442
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/066,029
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BHAVSAR, SUNIL
TITLE OF INVENTION: USE OF EXENDING AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/10/187,051
CURRENT FILING DATE: 2002-66-28
CURRENT FILING DATE: 2002-66-28
                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US/09/003,869
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 60/034,905
PRIOR FILING DATE: 1997-01-07
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                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
ORGANISM: Artificial Sequence
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BHAVSAR, SUNIL
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RESULT 26
US-09-003-869-69
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US-09-756-690A-11
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APPLICANT: KOLTERMAN, ORVILLE G. APPLICANT: YOUNG, ANDREW A.
                                                                                                                                                                          Sequence 69, Application US/09003869A
Patent No. US20020137666A1
GENERAL INFORMATION:
APPLICANT: BEELEY, NIGEL ROBERT ARNOLD
APPLICANT: PRICKETT, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver 2.1
SEQ ID NO 11
LENGTH: 38
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                 TITLE OF INVENTION: USE OF EXEMDINS AND AGONISTS TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE FILE REFERENCE: 23/1/81
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
CURRENT FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
EARLIER APPLICATION NUMBER: US 60/055,404
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LOCATION: (39)...(39)
OTHER INFORMATION: amidated Ser (Serinamide)
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Local Similarity 62.5%;
es 20; Conservative
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54.8%;

 Mismatches

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Pred. No. 7.
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Pred. No. 6.3e-06;
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APPLICANT: BELEY, NIGEL ROBERT ARNOLD
APPLICANT: BELEY, KATHRYN S.
APPLICANT: BHAVSAR, SUNIL
ITILE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR
TITLE OF INVENTION: THE REDUCTION OF FOOD INTAKE
FILE REFERENCE: 231/181
CURRENT APPLICATION NUMBER: US/09/003,869A
CURRENT APPLICATION NUMBER: US 60/034,905
EARLIER APPLICATION NUMBER: US 60/034,905
EARLIER FILING DATE: 1997-01-07
EARLIER APPLICATION NUMBER: US 60/055,404
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 198
CONTENTS ESC ID NOS: 198
밁
                                                                                                                                                                                                     US-09-003-869-173
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EARLIER APPLICATION NUMBER: US 60/065,442
EARLIER FILING DATE: 1997-11-14
EARLIER APPLICATION NUMBER: US 60/066,029
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 188
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                   Matches
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                        OTHER INFORMATION: amidated Ala (Alaninamide)
                                                                                                                                                                                                                                                   NAME/KEY: AMIDATION LOCATION: (35)...(3)
                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: artificially synthesized sequence of novel exendin agonist OTHER INFORMATION: compound
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: amidated Ala (Alaninamide)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Local Similarity 59.4%;
es 19; Conservative
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  4 GTFTSDLSKQLEEEAVRLFIEFLKNGGPSSGA 35
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ilarity 59.4%;
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Pred. No. 8.6e-06;
                                                                                                                      Score 69.5; DB 10
Pred. No. 8.6e-06
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FILE REFERENCE: 249/124
CUURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver 2.1
SEQ ID NO 69
LENGTH: 35
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US-09-756-690A-69
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US-09-756-690A-173
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                                                                                                                                                                                                                                                                                                                                                              Sequence 173, Application US/09756690A
Publication No. US20030036504A1
GENERAL INFORMATION:
APPLICANT: KOLTERMAN, ORVILLE G.
APPLICANT: YOUNG, ANDREW A.
TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF
TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
FILL REFERENCE: 249/124
FULLE REFERENCE: 249/124
CURRENT APPLICATION NUMBER: US/09/756,690A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin Ver 2.1
SEQ ID NO 173
FENCTU. 35
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Publication No. US20030036504A1

GENERAL INFORMATION:

APPLICANT: KOLTERMAN, ORVILLE G.

APPLICANT: YOUNG, ANDREW A.

TITLE OF INVENTION: USE OF EXENDINS AND AGONISTS THEREOF FOR MODULATION OF

TITLE OF INVENTION: TRIGLYCERIDE LEVELS AND TREATMENT OF DYSLIPIDEMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                       Query Match
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                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Exendin Agonist FEATURE:
                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                             OTHER INFORMATION: c-term amidation
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Local Similarity 59.4%;
les 19; Conservative (
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                                          4 GTXXXXXSKQXEEEAVRLXXXXL-XGGXSSGA 34
                                                                                                                   Similarity
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GTFTSDLSKOLEEEAVRLFIEFLKNGGPSSGA 35
                                                                                          Conservative
                                                                                                              62.1%;
                                                                                          0
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                                                                                       Score 69.5; DB 11
Pred. No. 8.6e-06;
0; Mismatches 12
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Pred. No. 8.6e-06
                                                                                                                                    DB 11;
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                                                                                          Gaps
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RESULT 30 US-10-157-224A-69

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Sequence 69, Application US/1015724A
Publication No. US20030087820A1
GENERAL INFORMATION:
APPLICANT: YOUNG, ANDREW A.
APPLICANT: YOUNG AND STRAIN THEREOF
FILLE REFERENCE: 02001-050
CURRENT APPLICATION NUMBER: US/10/157,224A
CURRENT FILING DATE: 2000-05-28
JERIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/116,380
PRIOR APPLICATION NUMBER: 60/175,365
PRIOR PRILING DATE: 2000-01-10
NUMBER OF SEQ 1D NOS: 188
SOFTWARE: PATENTION: C-term amidation
US-10-157-224A-69
PRIOR TIME INFORMATION: C-term amidation
US-10-157-224A-69
PRIOR TIME INFORMATION: C-term amidation
US-10-157-224A-69
PRIOR APPLICATION NUMBER: 60.1%; Score 69.5; DB 15; Length 35;
Best Local Similarity 59.4%; Pred. No. 8.6e-06;
PRIOR ENTRY OF THE PRICE OF THE PRIOR NUMBER: 60.1%; Score 69.5; DB 15; Length 35;
PRIOR APPLICATION NUMBER: 60.1%; Score 69.5; DB 15; Length 35;
PRIOR APPLICATION NUMBER: 60.1%; Score 69.5; DB 15; Length 35;
PRIOR APPLICATION NUMBER: 60/175, 365
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